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(71) Applicant *(for all designated States except US)*: **INFECTIO DIAGNOSTIC (I.D.I.) INC.** [CA/CA]; 2050 René-Lévesque Blvd. Ouest, 4th Floor, Sainte-Foy, Quebec G1V 2K8 (CA).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **HULETSKY, Ann** [CA/CA]; 1231 des Pins Avenue, Sillery, Quebec G1S 4J3 (CA). **ROSSBACH, Valery** [CA/CA]; 55 rue du Sauternes, Aylmer, Quebec J9H 3W7 (CA).

(74) Agents: **DUBUC, J., Prince** et al.; Goudreau Gage Dubuc, Stock Exchange Tower, Suite 3400, 800 Place Victoria, P.O. Box 242, Montréal, Québec H4Z 1E9 (CA).

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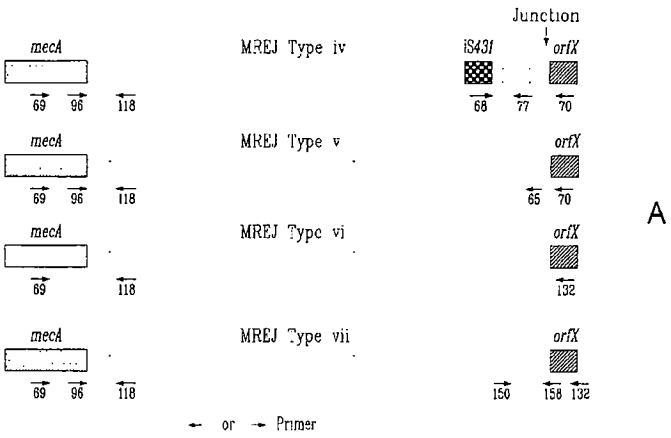
(54) Title: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCCOCUS AUREUS*



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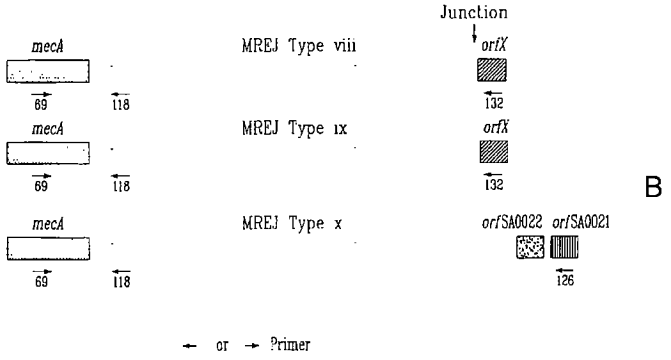

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(57) Abstract: The present invention describes novel SCC*mec* right extremity junction sequences for the detection of methicillin-resistant *Staphyloccocus aureus* (MRSA). It relates to the use of these DNA sequences for diagnostic purposes.

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SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS*

BACKGROUND OF THE INVENTION

Clinical significance of *Staphylococcus aureus*

The coagulase-positive species *Staphylococcus aureus* is well documented as a human opportunistic pathogen. Nosocomial infections caused by *S. aureus* are a major cause of morbidity and mortality. Some of the most common infections caused by *S. aureus* involve the skin, and they include furuncles or boils, cellulitis, impetigo, and postoperative wound infections at various sites. Some of the more serious infections produced by *S. aureus* are bacteremia, pneumonia, osteomyelitis, acute endocarditis, myocarditis, pericarditis, cerebritis, meningitis, scalded skin syndrome, and various abcesses. Food poisoning mediated by staphylococcal enterotoxins is another important syndrome associated with *S. aureus*. Toxic shock syndrome, a community-acquired disease, has also been attributed to infection or colonization with toxigenic *S. aureus* (Murray *et al.* Eds, 1999, Manual of Clinical Microbiology, 7th Ed., ASM Press, Washington, D.C.).

Methicillin-resistant *S. aureus* (MRSA) emerged in the 1980s as a major clinical and epidemiologic problem in hospitals. MRSA are resistant to all β-lactams including penicillins, cephalosporins, carbapenems, and monobactams, which are the most commonly used antibiotics to cure *S. aureus* infections. MRSA infections can only be treated with more toxic and more costly antibiotics, which are normally used as the last line of defence. Since MRSA can spread easily from patient to patient via personnel, hospitals over the world are confronted with the

problem to control MRSA. Consequently, there is a need to develop rapid and simple screening or diagnostic tests for detection and/or identification of MRSA to reduce its dissemination and improve the diagnosis and treatment of infected patients.

Methicillin resistance in *S. aureus* is unique in that it is due to acquisition of DNA from other coagulase-negative staphylococci (CNS), coding for a surnumerary β-lactam-resistant penicillin-binding protein (PBP), which takes over the biosynthetic functions of the normal PBPs when the cell is exposed to β-lactam antibiotics. *S. aureus* normally contains four PBPs, of which PBPs 1, 2 and 3 are essential. The low–affinity PBP in MRSA, termed PBP 2a (or PBP2'), is encoded by the choromosomal *mecA* gene and functions as a β-lactam-resistant transpeptidase. The *mecA* gene is absent from methicillin-sensitive *S. aureus* but is widely distributed among other species of staphylococci and is highly conserved (Ubukata *et al.,* 1990, Antimicrob. Agents Chemother. **34:**170-172).

By nucleotide sequence determination of the DNA region surrounding the *mecA* gene from *S. aureus* strain N315 (isolated in Japan in 1982), Hiramatsu *et al.* have found that the *mecA* gene is carried by a novel genetic element, designated staphylococcal cassette chromosome *mec* (SCC*mec*), inserted into the chromosome. SCC*mec* is a mobile genetic element characterized by the presence of terminal inverted and direct repeats, a set of site-specific recombinase genes (*ccrA* and *ccrB*), and the *mecA* gene complex (Ito *et al.,* 1999, Antimicrob. Agents Chemother. **43**:1449-1458; Katayama *et al.,* 2000, Antimicrob. Agents Chemother. **44**:1549-1555). The element is precisely excised from the chromosome of *S. aureus* strain N315 and integrates into a specific *S. aureus* chromosomal site in the same orientation through the function of a unique set of recombinase genes comprising *ccrA* and *ccrB*. Two novel genetic elements that shared similar structural features of SCC*mec* were found by cloning and sequencing the DNA

region surrounding the *mecA* gene from MRSA strains NCTC 10442 (the first MRSA strain isolated in England in 1961) and 85/2082 (a strain from New Zealand isolated in 1985). The three SCC*mec* have been designated type I (NCTC 10442), type II (N315) and type III (85/2082) based on the year of isolation of the strains (Ito *et al.,* 2001, Antimicrob. Agents Chemother. **45**:1323-1336) (Figure 1). Hiramatsu *et al.* have found that the SCC*mec* DNAs are integrated at a specific site in the methicillin-sensitive *S. aureus* (MSSA) chromosome. They characterized the nucleotide sequences of the regions around the left and right boundaries of SCC*mec* DNA (i.e. *att*L and *att*R, respectively) as well as those of the regions around the SCC*mec* DNA integration site (i.e. *attBscc* which is the bacterial chromosome attachment site for SCC*mec* DNA). The *attBscc* site was located at the 3' end of a novel open reading frame (ORF), *orfX*. The *orfX* potentially encodes a 159-amino acid polypeptide sharing identity with some previously identified polypeptides, but of unknown function (Ito *et al.,* 1999, Antimicrob. Agents Chemother. **43**:1449-1458). Recently, a new type of SCC*mec* (type IV) has been described by both Hiramatsu *et al.* (Ma *et al*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) and Oliveira *et al.* (Oliveira *et al*, 2001, Microb. Drug Resist. 7:349-360). The sequences of the right extremity of the new type IV SCC*mec* from *S. aureus* strains CA05 and 8/6-3P published by Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) were nearly identical over 2000 nucleotides to that of type II SCC*mec* of *S. aureus* strain N315 (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336). No sequence at the right extremity of the SCC*mec* type IV is available from the *S. aureus* strains HDE288 and PL72 described by Oliveira *et al.* (Oliveira *et al.*, 2001, Microb.Drug Resist. 7:349-360).

Previous methods used to detect and identify MRSA (Saito *et al.,* 1995, J. Clin. Microbiol. **33**:2498-2500; Ubukata *et al.,* 1992, J. Clin. Microbiol. **30**:1728-1733; Murakami *et al.,* 1991, J. Clin. Microbiol. **29**:2240-2244; Hiramatsu *et al.*, 1992,

Microbiol. Immunol. **36**:445-453), which are based on the detection of the *mecA* gene and *S. aureus*-specific chromosomal sequences, encountered difficulty in discriminating MRSA from methicillin-resistant coagulase-negative staphylococci (CNS) because the *mecA* gene is widely distributed in both *S. aureus* and CNS species (Suzuki *et al.,* 1992, Antimicrob. Agents. Chemother. **36**:429-434). Hiramatsu *et al.* (US patent 6,156,507) have described a PCR assay specific for MRSA by using primers that can specifically hybridize to the right extremities of the 3 types of SCC*mec* DNAs in combination with a primer specific to the *S. aureus* chromosome, which corresponds to the nucleotide sequence on the right side of the SCC*mec* integration site. Since nucleotide sequences surrounding the SCC*mec* integration site in other staphylococcal species (such as *S. epidermidis* and *S. haemolyticus*) are different from those found in *S. aureus*, this PCR assay was specific for the detection of MRSA. This PCR assay also supplied information for MREP typing (standing for «*mec* right extremity polymorphism») of SCC*mec* DNA (Ito *et al.,* 2001, Antimicrob. Agents Chemother. **45**:1323-1336; Hiramatsu *et al.,* 1996, J. Infect. Chemother. **2**:117-129). This typing method takes advantage of the polymorphism at the right extremity of SCC*mec* DNAs adjacent to the integration site among the three types of SCC*mec*. Type III has a unique nucleotide sequence while type II has an insertion of 102 nucleotides to the right terminus of SCC*mec* type I. The MREP typing method described by Hiramatsu*et al.* (Ito *et al.,* 2001, Antimicrob. Agents Chemother. **45**:1323-1336; Hiramatsu *et al.,* 1996, J. Infect. Chemother. **2**:117-129) defines the SCC*mec* type I as MREP type i, SCC*mec* type II as MREP type ii and SCC*mec* type III as MREP type iii. It should be noted that the MREP typing method cannot differentiate the new SCC*mec*type IV described by Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) from SCC*mec* type II because these two SCC*mec* types exhibit the same nucleotide sequence to the right extremity.

The set of primers described by Hiramatsu et al. as being the optimal primer combination (SEQ ID NOs.: 22, 24, 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) have been used in the present invention to test by PCR a variety of MRSA and MSSA strains (Figure 1 and Table 1). Twenty of the 39 MRSA strains tested were not amplified by the Hiramatsu et al. multiplex PCR assay (Tables 2 and 3). Hiramitsu's method indeed was successful in detecting less than 50% of the tested 39 MRSA strains. This finding demonstrates that some MRSA strains have sequences at the right extremity of SCC*mec*-chromosome right extremity junction different from those identified by Hiramatsu *et al.* Consequently, the system developed by Hiramatsu *et al.* does not allow the detection of all MRSA. The present invention relates to the generation of SCC*mec*-chromosome right extremity junction sequence data required to detect more MRSA strains in order to improve the Hiramatsu *et al.* assay. There is a need for developing more ubiquitous primers and probes for the detection of most MRSA strains around the world.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids from all MRSA strains.

Ubiquity of at least 50% amongst the strains representing MRSA strains types IV to X is an objective of this invention.

Therefore, in accordance with the present invention is provided a method to detect the presence of a methicillin-resistant *Staphylococcus aureus* (MRSA) strain in a sample, the MRSA strain being resistant because of the presence of an SCC*mec*

insert containing a mecA gene, said SCC*mec* being inserted in bacterial nucleic acids thereby generating a polymorphic right extremity junction (MREJ), the method comprising the step of annealing the nucleic acids of the sample with a plurality of probes and/or primers, characterized by:

(i) the primers and/or probes are specific for MRSA strains and capable of annealing with polymorphic MREJ nucleic acids, the polymorphic MREJ comprising MREJ types i to x; and

(ii) the primers and/or probes altogether can anneal with at least four MREJ types selected from MREJ types i to x.

In a specific embodiment, the primers and/or probes are all chosen to anneal under common annealing conditions, and even more specifically, they are placed altogether in the same physical enclosure.

A specific method has been developed using primers and/or probes having at least 10 nucleotides in length and capable of annealing with MREJ types i to iii, defined in any one of SEQ ID NOs: 1, 20, 21, 22, 23, 24, 25, 41, 199 ; 2, 17, 18, 19, 26, 40, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 185, 186, 197 ; 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 104, 184, 198 and with one or more of MREJ types iv to ix, having SEQ ID NOs: 42, 43, 44, 45, 46, 51 ; 47, 48, 49, 50 ; 171 ; 165, 166 ; 167 ; 168. To be perfectly ubiquitous with the all the sequenced MREJs, the primers and/or probes altogether can anneal with said SEQ ID NOs of MREJ types i to ix.

The following specific primers and/or probes having the following sequences have been designed:

66, 100, 101, 105, 52, 53, 54, 55, 56, 57, 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159, 59, 62, 126, 127, 128, 129, 131, 200, 201, 60, 61, 63	for the detection of MREJ type i
32, 83, 84, 160, 161, 162, 163, 164	
85, 86, 87, 88, 89	

66, 97, 99, 100, 101, 106, 117, for the detection of MREJ type ii
118, 124, 125, 52, 53, 54, 55, 56, 57
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

67, 98, 102, 107, 108 for the detection of MREJ type iii
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
58,
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

79, 77, 145, 147 for the detection of MREJ type iv
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
68
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

65, 80, 146, 154, 155 for the detection of MREJ type v
64, 71, 72, 73, 74, 75, 76,
70, 103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

202, 203, 204 for the detection of MREJ type vi
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

112, 113, 114, 119, 120, 121, 122 for the detection of MREJ type vii,
123, 150, 151, 153
64, 71, 72, 73, 74, 75, 76, 70, 103,
130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

115, 116, 187, 188, 207, 208 for the detection of MREJ type viii
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

109, 148, 149, 205, 206 for the detection of MREJ type ix.
64, 71, 72, 73, 74, 75, 76
70, 103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

Amongst these, the following primer pairs having the following sequences are used:

64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57	for the detection of type i MREJ
64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57	for the detection of type ii MREJ
64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58	for the detection of type iii MREJ
64/79	for the detection of type iv MREJ
64/80	for the detection of type v MREJ
64/204	for the detection of type vi MREJ
64/112, 64/113	for the detection of type vii MREJ
64/115, 64/116	for the detection of type viii MREJ
64/109	for the detection of type ix MREJ

As well, amongst these, the following probes having the following sequences are used:

SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164 for the detection of MREJ types i to ix.

In the most preferred embodied method, the following primers and/or probes having the following nucleotide sequences are used together. The preferred combinations make use of:

i) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type i
ii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type ii
iii) SEQ ID NOs: 64, 67, 84, 163, 164 for the detection of MREJ type iii
iv) SEQ ID NOs: 64, 79, 84, 163, 164 for the detection of MREJ type iv
v) SEQ ID NOs: 64, 80, 84, 163, 164 for the detection of MREJ type v
vi) SEQ ID NOs: 64, 112, 84, 163, 164 for the detection of MREJ type vii.

All these probes and primers can even be used together in the same physical enclosure.

It is another object of this invention to provide a method for typing a MREJ of a MRSA strain, which comprises the steps of: reproducing the above method with primers and/or probes specific for a determined MREJ type, and detecting an annealed probe or primer as an indication of the presence of a determined MREJ type.

It is further another object of this invention to provide a nucleic acid selected from SEQ ID NOs:

i) SEQ ID NOs: 42, 43, 44, 45, 46, 51 for sequence of MREJ type iv ;
ii) SEQ ID NOs: 47, 48, 49, 50 for sequence of MREJ type v ;
iii) SEQ ID NOs: 171 for sequence of MREJ type vi ;
iv) SEQ ID NOs: 165, 166 for sequence of MREJ type vii ;
v) SEQ ID NOs: 167 for sequence of MREJ type viii ;
vi) SEQ ID NOs: 168 for sequence of MREJ type ix.

Oligonucleotides of at least 10 nucleotides in length which hybridize with any of these nucleic acids and which hybridize with one or more MREJ of types selected from iv to ix are also objects of this invention. Amongst these, primer pairs (or probes) having the following SEQ ID NOs:

64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57	for the detection of type i MREJ
64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57	for the detection of type ii MREJ
64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58	for the detection of type iii MREJ
64/79	for the detection of type iv MREJ
64/80	for the detection of type v MREJ
64/204	for the detection of type vi MREJ
64/112, 64/113	for the detection of type vii MREJ
64/115, 64/116	for the detection of type viii MREJ
64/109	for the detection of type ix MREJ,

are also within the scope of this invention.

Further, internal probes having nucleotide sequences defined in any one of SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164, are also within the scope of this invention. Compositions of matter comprising the primers and/or probes annealing or hybridizing with one or more MREJ of types selected from iv to ix as well as with the above nucleic acids, comprising or not primers and/or probes, which hybridize with one or more MREJ of types selected from i to iii, are further objects of this invention. The preferred compositions would comprise the primers having the nucleotide sequences defined in SEQ ID NOs:

64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57	for the detection of type i MREJ
64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57	for the detection of type ii MREJ
64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58	for the detection of type iii MREJ
64/79	for the detection of type iv MREJ
64/80	for the detection of type v MREJ
64/204	for the detection of type vi MREJ
64/112, 64/113	for the detection of type vii MREJ
64/115, 64/116	for the detection of type viii MREJ
64/109	for the detection of type ix MREJ,

or probes, which SEQ ID NOs are: 32, 83, 84, 160, 161, 162, 163, 164, or both.

DETAILED DESCRIPTION OF THE INVENTION

Here is particularly provided a method wherein each of MRSA nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said primers or probes developed to be ubiquitous;

wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said primers or probes ;

said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of MRSA.

In the method, sequences from DNA fragments of SCC*mec*-chromosome right extremity junction, therafter named MREJ standing for « *mec* right extremity junction » including sequences from SCC*mec* right extremity and chromosomal DNA to the right of the SCC*mec* integration site are used as parental sequences from which are derived the primers and/or the probes. MREJ sequences include our proprietary sequences as well as sequences obtained from public databases and from US patent 6,156,507 and were selected for their capacity to sensitively, specifically, ubiquitously and rapidly detect the targeted MRSA nucleic acids.

Our proprietary DNA fragments and oligonucleotides (primers and probes) are also another object of this invention.

Composition of matters such as diagnostic kits comprising amplification primers or probes for the detection of MRSA are also objects of the present invention.

In the above methods and kits, probes and primers are not limited to nucleic acids and may include, but are not restricted to, analogs of nucleotides. The diagnostic reagents constitued by the probes and the primers may be present in any suitable form (bound to a solid support, liquid, lyophilized, etc.).

In the above methods and kits, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence replication (3SR), e) strand displacement amplification (SDA), f) branched DNA signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCA), n) Anchored strand displacement amplification, o) Solid-phase (immobilized) rolling circle amplification.

In the above methods and kits, detection of the nucleic acids of target genes may include real-time or post-amplification technologies. These detection technologies can include, but are not limited to fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization of probes (including probe-probe and probe-primer methods), *Taq*Man probe, molecular beacon probe, Scorpion probe, nanoparticle probe and Amplifluor probe. Other detection methods include target gene nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support. In these systems, the hybridization can be monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, flow cytometry or scanometry. Nucleotide sequencing, including sequencing by dideoxy termination or sequencing by hybridization (e.g. sequencing using a DNA

chip) represents another method to detect and characterize the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification.

A method for detection of a plurality of potential MRSA strains having different MREJ types may be conducted in separate reactions and physical enclosures, one type at the time. Alternatively, it could be conducted simultaneously for different types in separate physical enclosures, or in the same physical enclosures. In the latter scenario a multiplex PCR reaction could be conducted which would require that the oligonucleotides are all capable of annealing with a target reagion under common conditions. Since many probes or primers are specific for a determined MREJ type, typing a MRSA strain is a possible embodiment. When a mixture of oligonucleotides annealing together with more than one type is used in a single physical enclosure or container, different labels would be used to distinguish one type from another.

We aim at developing a DNA-based test or kit to detect and identify MRSA. Although the sequences from *orfX* genes and some SCC*mec* DNA fragments are available from public databases and have been used to develop DNA-based tests for detection of MRSA, new sequence data allowing to improve MRSA detection and identification which are object of the present invention have either never been characterized previously or were known but not shown to be located at the right extremity of *SCCmec* adjacent to the integration site (Table 4). These novel sequences could not have been predicted nor detected by the MRSA-specific PCR assay developed by Hiramatsu *et al.* (US patent 6,156,507). These sequences will allow to improve current DNA-based tests for the diagnosis of MRSA because they allow the design of ubiquitous primers and probes for the detection and

identification of more MRSA strains including all the major epidemic clones from around the world.

The diagnostic kits, primers and probes mentioned above can be used to detect and/or identify MRSA, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environmental sample, any microbial culture, any microbial colony, any tissue, and any cell line.

It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in combination with any other assay suitable to detect and/or identify microorganisms, including but not limited to: any assay based on nucleic acids detection, any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration cuture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA sequences have been obtained either from our proprietary sequences or from public databases (Tables 5, 6, 7, 8 and 9).

It is clear to the individual skilled in the art that oligonucleotide sequences other than those described in the present invention and which are appropriate for detection and/or identification of MRSA may also be derived from the proprietary fragment sequences or selected public database sequences. For example, the

oligonucleotide primers or probes may be shorter but of a lenght of at least 10 nucleotides or longer than the ones chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may also be variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from said DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the detection and/or identification of MRSA by targeting genomic DNA sequences which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes require much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Tables 5, 6, 7, 8 and 9 which are suitable for diagnostic purposes. When a proprietary fragment or a public database sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

The proprietary DNA fragments have been obtained as a repertory of sequences created by amplifying MRSA nucleic acids with new primers. These primers and the repertory of nucleic acids as well as the repertory of nucleotide sequences are further objects of this invention (Tables 4, 5, 6, 7, 8 and 9).

Claims therefore are in accordance with the present invention.

SEQUENCES FOR DETECTION AND IDENTIFICATION OF MRSA

In the description of this invention, the terms «nucleic acids» and «sequences» might be used interchangeably. However, «nucleic acids» are chemical entities while «sequences» are the pieces of information encoded by these «nucleic acids». Both nucleic acids and sequences are equivalently valuable sources of information for the matter pertaining to this invention.

Oligonucleotide primers and probes design and synthesis

As part of the design rules, all oligonucleotides (probes for hybridization and primers for DNA amplification by PCR) were evaluated for their suitability for hybridization or PCR amplification by computer analysis using standard programs (i.e. the GCG Wisconsin package programs, the primer analysis softwareOligo™ 6 and MFOLD 3.0). The potential suitability of the PCR primer pairs was also evaluated prior to their synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Oligonucleotide amplification primers were synthesized using an automated DNA synthesizer (Applied Biosystems). Molecular beacon designs were evaluated using criteria established by Kramer *et al.* (http://www.molecular-beacons.org).

The oligonucleotide sequence of primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s) (Nichols *et al.*, 1994, Nature **369**:492-493). Primers and probes may also consist of nucleotide analogs such as Locked Nucleic Acids (LNA) (Koskin*et*

al., 1998, Tetrahedron **54**:3607-3630), and Peptide Nucleic Acids (PNA) (Egholm *et al.*, 1993, Nature **365**:566-568). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments, or from selected database sequences which are suitable for the detection of MRSA.

Variants for a given target microbial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson*et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same microbial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant nucleic acids and/or sequences for a specific gene and that the frequency of sequence variations depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variations at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this primer hybridization site. A similar strategy may be applied to show variations at the hybridization site of a probe. Insofar as the divergence of the target nucleic acids and/or sequences or a part thereof does not affect significantly the sensitivity and/or specificity and/or ubiquity of the amplification primers or probes, variant microbial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant target DNA.

DNA amplification

For DNA amplification by the widely used PCR method, primer pairs were derived from our proprietary DNA fragments or from public database sequences.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing *et al*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols on a standard thermocycler (PTC-200 from MJ Research Inc., Watertown, MA) were as follows: Treated standardized bacterial suspensions or genomic DNA prepared from bacterial cultures or clinical specimens were amplified in a 20 µl PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM $MgCl_2$, 0.4 µM of each primer, 200 µM of each of the four dNTPs (Pharmacia Biotech), 3.3 µg/µl bovine serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada) and 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI) combined with the *Taq*Start™antibody (BD Biosciences, Palo Alto, CA). The *Taq*Start™ antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the amplifications (Kellogg *et al.*, 1994, Biotechniques **16**:1134-1137). The treatment of bacterial cultures or of clinical specimens consists in a rapid protocol tolyse the microbial cells and eliminate or neutralize PCR inhibitors (described in co-pending application US 60/306,163). For amplification from purified genomic DNA, the samples were added directly to the PCR amplification mixture. An internal control,

derived from sequences not found in the target MREJ sequences or in the human genome, was used to verify the efficiency of the PCR reaction and the absence of significant PCR inhibition.

The number of cycles performed for the PCR assays varies according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from a clinical specimen is higher than for detection from a microbial culture. Consequently, more sensitive PCR assays having more thermal cycles are probably required for direct detection from clinical specimens.

The person skilled in the art of nucleic acid amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), reverse transcriptase PCR (RT-PCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling circle amplification technology (RCA), solid phase RCA, anchored SDA and nuclease dependent signal amplification (NDSA) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.;Westin *et al.*, 2000, Nat. Biotechnol. 18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any nucleic acid amplification method or any other procedure which may be used to increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or array technologies, any amplification chips or

combination of amplification and hybridization chip technologies. Detection and identification by any nucleotide sequencing method is also under the scope of the present invention.

Any oligonucleotide derived from the *S. aureus* MREJ DNA sequences and used with any nucleic acid amplification and/or hybridization technologies are also under the scope of this invention.

Evaluation of the MRSA detection method developed by Hiramatsu *et al.*

According to Hiramatsu *et al.* (Ito *et al.,* 1999, Antimicrob. Agents Chemother. **43**:1449-1458; Katayama *et al.,* 2000, Antimicrob. Agents Chemother. **44**:1549-1555; Ito *et al.,* 2001, Antimicrob. Agents Chemother. **45**:1323-1336, Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152), four types of SCC*mec* DNA are found among MRSA strains. They have found that SCC*mec* DNAs are integrated at a specific site of the MSSA chromosome (named *orfX*). They developed a MRSA-specific multiplex PCR assay including primers that can hybridize to the right extremity of SCC*mec* types I, II and III (SEQ ID NOs.: 18, 19, 20, 21, 22, 23, 24 in US patent 6,156,507 corresponding to SEQ IDNOs.: 52, 53, 54, 55, 56, 57, 58, respectively, in the present invention) as well as primers specific to the *S. aureus* chromosome to the right of the SCC*mec* integration site (SEQ ID NO.: 25, 28, 27, 26, 29 in US patent 6,156,507 corresponding to SEQ ID NOs.: 59, 60, 61, 62, 63, respectively, in the present invention) (Table 1 and Figure 1). The set of primers described by Hiramatsu *et al.* as being the optimal primer combination (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) was used in the present invention to test by PCR a variety of MRSA, MSSA, methicillin-resistant CNS (MRCNS) and methicillin-sensitive CNS (MSCNS) strains (Table 2). A PCR assay performed using a standard thermocycler (PTC-200 from MJ Research Inc.) was

used to test the ubiquity, the specificity and the sensitivity of these primers using the following protocol: one µl of a treated standardized bacterial suspension or of a genomic DNA preparation purified from bacteria were amplified in a 20 µl PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.4 µM of each of the SCC*mec*- and *S. aureus* chromosome-specific primers (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention), 200 µM of each of the four dNTPs (Pharmacia Biotech), 3.3 µg/µl BSA (Sigma), and 0.5 U *Taq* polymerase (Promega) coupled with *Taq*Start™ Antibody (BD Biosciences).

PCR reactions were then subjected to thermal cycling 3 min at 94°C followed by 40 cycles of 60 seconds at 95°C for the denaturation step, 60 seconds at 55°C for the annealing step, and 60 seconds at 72°C for the extension step, then followed by a terminal extension of 7 minutes at 72°C using a standardthermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml ofethidium bromide. Twenty of the 39 MRSA strains tested were not amplified with the PCR assay developed by Hiramatsu *et al.* (Example 1, Tables 2 and 3).

With a view of establishing a rapid diagnostic test for MRSAs, the present inventors developed new sets of primers specific to the right extremity ofSCCmec types I and II (SEQ ID NOs.: 66, 100 and 101) (Annex 1), SCCmec type II (SEQ ID NOs.: 97 and 99), SCCmec type III (SEQ ID NOs.: 67, 98 and 102) and in the S. aureus chromosome to the right of the SCCmec integration site (SEQ ID NOs.: 64, 70, 71, 72, 73, 74, 75 and 76) (Table 5). These primers, amplifying short amplicons (171 to 278 bp), are compatible for use in rapid PCR assays (Table 7). The design of these primers was based on analysis of multiple sequence alignments of orfX and SCCmec sequences described by Hiramatsu et al. (US patent

6,156,507) or available from GenBank (Table 10, Annex I). These different sets of primers were used to test by PCR a variety of MRSA, MSSA, MRCNS and MSCNS strains. Several amplification primers were developed to detect all three SCCmec types (SEQ ID NOs.: 97 and 99 for SCCmec type II, SEQ ID NOs.: 66, 100 and 101 for SCCmec types I and II and SEQ ID NOs.: 67, 98 and 102 for SCCmec type III). Primers were chosen according to their specificity for MRSA strains, their analytical sensitivity in PCR and the length of the PCR product. A set of two primers was chosen for the SCCmec right extremity region (SEQ ID NO.: 66 specific to SCCmec types I and II; SEQ ID NO.: 67 specific to SCCmec type III). Of the 8 different primers designed to anneal on the S.aureus chromosome to the right of the SCCmec integration site (targeting orfX gene) (SEQ ID NOs.: 64, 70, 71, 72, 73, 74, 75 and 76), only one (SEQ ID.: 64) was found to be specific for MRSA based on testing with a variety of MRSA, MSSA, MRCNS and MSCNS strains (Table 12). Consequently, a PCR assay using the optimal set of primers (SEQ ID NOs.: 64, 66 and 67) which could amplify specifically MRSA strains containing SCCmec types I, II and III was developed (Figure 2, Annex I). While the PCR assay developed with this novel set of primers was highly sensitive (i.e allowed the detection of 2 to 5 copies of genome for all three SCCmec types) (Table 11), it had the same shortcomings (i.e. lack of ubiquity) of the test developed by Hiramatsu et al. The 20 MRSA strains which were not amplified by the Hiramatsu et al. primers were also not detected by the set of primers comprising SEQ ID NOs.: 64, 66 and 67 (Tables 3 and 12). Clearly, diagnostic tools for achieving at least 50% ubiquity amongst the tested strains are needed.

With a view to establish a more ubiquitous (i.e. ability to detect all or most MRSA strains) detection and identification method for MRSA, we determined the sequence of the MREJ present in these 20 MRSA strains which were not amplified. This research has led to the discovery and identification of seven novel distinct MREJ target sequences which can be used for diagnostic purposes. These

seven new MREJ sequences could not have been predicted nor detected with the system described in US patent 6,156,507 by Hiramatsu *et al.* Namely, the present invention represents an improved method for the detection and identification of MRSA because it provides a more ubiquitous diagnostic method which allows for the detection of all major epidemic MRSA clones from around the world.

Sequencing of MREJ nucleotide sequences from MRSA strains not amplifiable with primers specific to SCC*mec* types I, II and III

Since DNA from twenty MRSA strains were not amplified with the set of primers developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) (Tables 2 and 3) nor with the set of primers developed in the present invention based on the same three SCC*mec* types (I, II and III) sequences (SEQ ID NOs.: 64, 66 and 67) (Table 12), the nucleotide sequence of the MREJ was determined for sixteen of these twenty MRSA strains.

Transposase of IS*431* is often associated with the insertion of resistance genes within the *mec* locus. The gene encoding this transposase has been described frequently in one or more copies within the right segment of SCC*mec* (Oliveira *et al.*, 2000, Antimicrob. Agents Chemother. **44**:1906-1910; Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-36). Therefore, in a first attempt to sequence the novel MREJ for 16 of the 20 MRSA strains described in Table 3, a primer was designed in the sequence of the gene coding for the transposase of IS*431* (SEQ ID NO.: 68) and combined with an *orfX*-specific primer to the right of the SCC*mec* integration site (SEQ ID NO.: 70) (Tables 5 and 8). The strategy used to select these primers is illustrated in Figure 3.

The MREJ fragments to be sequenced were amplified using the following amplification protocol: one µL of treated cell suspension (or of a purifiedgenomic DNA preparation) was transferred directly into 4 tubes containing 39 µL of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 1 µM of each of the 2 primers (SEQ ID NOs.: 68 and 70), 200 µM of each of the four dNTPs, 3.3 µg/µl of BSA (Sigma-Aldrich Canada Ltd) and 0.5 unit of *Taq* DNA polymerase (Promega) coupled with the *Taq*Start™ Antibody (BD Bisociences). PCR reactions were submitted to cycling using a standard thermocycler (PTC-200 from MJ Research Inc.) as follows: 3 min at 94 °C followed by 40 cycles of 5 sec at 95 °C for the denaturation step, 30 sec at 55 °C for the annealing step and 2 min at 72 °C for the extension step.

Subsequently, the four PCR-amplified mixtures were pooled and 10 µL of the mixture were resolved by electrophoresis in a 1.2% agarose gel containing 0.25µg/mL of ethidium bromide. The amplicons were then visualized with an Alpha-Imager (Alpha Innotech Corporation, San Leandro, CA) by exposing to UV light at 254 nm. Amplicon size was estimated by comparison with a 1 kb molecular weight ladder (Life Technologies, Burlington, Ontario, Canada). The remaining PCR-amplified mixture (150 µL, total) was also resolved by electrophoresis in a 1.2% agarose gel. The amplicons were then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, **13**:203-205). Amplicon size was once again estimated by comparison with a 1 kb molecular weight ladder. Of the sixteen strains selected from the twenty described in Table 3, six were amplified using SEQ ID NOs.: 68 and 70 as primers (CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504). For these six MRSA strains, an amplification product of 1.2 kb was obtained. Theband corresponding to this specific amplification product was excised from theagarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-

purified DNA fragment was then used directly in the sequencing protocol. Both strands of the MREJ amplification products were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 377) with their Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA). The sequencing reactions were performed by using the same primers (SEQ ID NOs.: 68 and 70) and 10 ng/100 bp per reaction of the gel-purified amplicons. Sequencing of MREJ from the six MRSA strains (CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504) described in Table 3 yielded SEQ ID NOs.: 42, 43, 44, 45, 46 and 51, respectively (Table 4).

In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified MREJ amplification products originating from two independent PCR amplifications. For most target fragments, the sequences determined for both amplicon preparations were identical. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The MREJ sequences determined using the above strategy are described in the Sequence Listing and in Table 4.

In order to sequence MREJ in strains for which no amplicon had been obtained using the strategy including primers specific to thetransposase gene of IS*431* and *orfX*, another strategy using primers targeting *mecA* and *orfX* sequences was used to amplify longer genomic fragments. A new PCR primer targeting *mecA* (SEQ ID NO.: 69) (Table 8) to be used in combination with the same primer in the *orfX* sequence (SEQ ID NO.: 70). The strategy used to select these primers is illustrated in Figure 3.

The following amplification protocol was used: Purified genomic DNA (300 ng) was transferred to a final volume of 50 µl of a PCR reaction mixture. Each PCR reaction contained 1X Herculase buffer (Stratagene, La Jolla, CA), 0.8 µM of each of the 2 primers (SEQ ID NOs.: 69 and 70), 0.56 mM of each of the four dNTPs and 5 units of *Herculase* (Stratagene). PCR reactions were subjected to cycling using a standard thermal cycler (PTC-200 from MJ Research Inc.) as follows: 2 min at 92 °C followed by 35 or 40 cycles of 10 sec at 92 °C for the denaturation step, 30 sec at 55 °C for the annealing step and 30 min at 68 °C for the extension step.

Subsequently, 10 µL of the PCR-amplified mixture were resolved by electrophoresis in a 0.7% agarose gel containing 0.25µg/mL of ethidium bromide. The amplicons were then visualized as described above. Amplicon size was estimated by comparison with a 1 kb molecular weight ladder (Life Technologies). A reamplification reaction was then performed in 2 to 5 tubes using the same protocol with 3 µl of the first PCR reaction used as test sample for the second amplification. The PCR-reamplified mixtures were pooled and also resolved by electrophoresis in a 0.7% agarose gel. The amplicons were then visualized by staining with methylene blue as described above. An amplification product of approximately 12 kb was obtained using this amplification strategy for all strains tested. The band corresponding to the specific amplification product was excised from the agarose gel and purified as described above. The gel-purified DNA fragment was then used directly in the sequencing protocol as described above. The sequencing reactions were performed by using the same amplification primers (SEQ ID NOs.: 69 and 70) and 425-495 ng of the gel-purified amplicons per reaction. Subsequently, internal sequencing primers (SEQ IDNOs.: 65, 77 and 96) (Table 8) were used to obtain sequence data on both strands for a larger portion of the amplicon. Five of the 20 MRSA strains (CCRI-1331, CCRI-1263, CCRI-1377, CCRI-1311 and CCRI-2025) described in Table 3 were sequenced using this

strategy, yielding SEQ ID NOs.: 46, 47, 48, 49 and 50, respectively (Table 4). Sequence within *mecA* gene was also obtained from the generated amplicons yielding SEQ ID NOs: 27, 28, 29, 30 and 31 from strains CCRI-2025, CCRI-1263, CCRI-1311, CCRI-1331 and CCRI-1377, respectively (Table 4). Longer sequences within the *mecA* gene and from downstream regions were also obtained for strains CCRI-2025, CCRI-1331, and CCRI-1377 as described below.

In order to obtain longer sequences of the *orfX* gene, two other strategies using primers targeting *mecA* and *orfX* sequences (at the start codon) was used to amplify longer chromosome fragments. A new PCR primer was designed in *orfX* (SEQ ID NO.: 132) to be used in combination with the same primer in the *mecA* gene (SEQ ID NO.: 69). The strategy used to select these primers is illustrated in Figure 3. Eight *S. aureus* strains were amplified using primers SEQ ID NOs.: 69 and 132 (CCRI-9860, CCRI-9208, CCRI-9504, CCRI-1331, CCRI-9583, CCRI-9681, CCRI-2025 and CCRI-1377). The strategy used to select these primers is illustrated in Figure 3.

The following amplification protocol was used: Purified genomic DNA (350 to 500 ng) was transferred to a 50 µl PCR reaction mixture. Each PCR reaction contained 1X Herculase buffer (Stratagene), 0.8 µM of each of the set of 2 primers (SEQ ID NOs.: 69 and 132), 0.56 mM of each of the four dNTPs and 7.5 units of *Herculase* (Stratagene) with 1 mM $MgCl_2$. PCR reactions were subjected to thermocycling as described above.

Subsequently, 5 µL of the PCR-amplified mixture were resolved by electrophoresis in a 0.8% agarose gel containing 0.25µg/mL of ethidium bromide. The amplicons were then visualized as described above. For one *S. aureus* strain (CCRI-9583), a reamplification was then performed by using primers SEQ ID NOs.: 96 and 158 (Figure 3) in 4 tubes, using the same PCR protocol, with 2 µl of

the first PCR reaction as test sample for the second amplification. The PCR-reamplified mixtures were pooled and also resolved by electrophoresis in a 0.8% agarose gel. The amplicons were then visualized by staining with methylene blue as described above. A band of approximately 12 to 20 kb was obtained using this amplification strategy depending on the strains tested. The band corresponding to the specific amplification product was excised from the agarose gel and purified using the QIAquick™ gel extraction kit or QIAEX II gel extraction kit (QIAGEN Inc.). Two strains, CCRI-9583 and CCRI-9589, were also amplified with primers SEQ ID NOs.: 132 and 150, generating an amplification product of 1.5 kb. Long amplicons (12-20 kb) were sequenced using 0.6 to 1 μg per reaction, while short amplicons (1.5 kb) were sequenced using 150 ng per reaction. Sequencing reactions were performed using different sets of primers for each *S. aureus* strain: 1) SEQ ID NOs.: 68, 70, 132, 145, 146, 147, 156, 157 and 158 for strain CCRI-9504; 2) SEQ ID NOs.: 70, 132, 154 and 155 for strain CCRI-2025; 3) SEQ ID NOs.: 70, 132, 148, 149, 158 and 159 for strain CCRI-9681; 4) SEQ IDNOs.: 70, 132, 187, and 188 for strain CCRI-9860; 5) SEQ IDNOs: 70, 132, 150 and 159 for strain CCRI-9589, 6) SEQ ID NOs.: 114, 123, 132, 150 and 158 for strain CCRI-9583; 7) SEQ ID NOs: 70, 132, 154 and 155 for strain CCRI-1377, 8) SEQ ID NOs.: 70, 132, 158 and 159 for strain CCRI-9208; 9) SEQ IDNOs: 68, 70, 132, 145, 146, 147 and 158 for strain CCRI-1331; and 10) SEQ IDNOs.: 126 and 127 for strain CCRI-9770.

In one strain (CCRI-9770), the *orfX* and *orf*SA0022 genes were shown to be totally or partially deleted based on amplification using primers specific to these genes (SEQ ID NOs: 132 and 159 and SEQ ID NOs.: 128 and 129, respectively) (Table 8). Subsequently, a new PCR primer was designed in *orf*SA0021 (SEQ ID NO.: 126) to be used in combination with the same primer in the *mecA* gene (SEQ ID NO.: 69). An amplification product of 4.5 kb was obtained with this primer set.

Amplification, purification of amplicons and sequencing of amplicons were performed as described above.

To obtain the sequence of the SSC*mec* region containing *mecA* for ten of the 20 MRSA strains described in Table 3 (CCRI-9504, CCRI-2025, CCRI-9208, CCRI-1331, CCRI-9681, CCRI-9860, CCRI-9770, CCRI-9589, CCRI-9583 and CCRI-1377), the primer described above designed in *mecA* (SEQ ID NO.: 69) was used in combination with a primer designed in the downstream region of *mecA* (SEQ ID NO.: 118) (Table 8). An amplification product of 2 kb was obtained for all the strains tested. For one strain, CCRI-9583, a re-amplification with primers SEQ ID NOs.: 96 and 118 was performed with the amplicon generated with primers SEQ ID NOs.: 69 and 132 described above. The amplication, re-amplification, purification of amplicons and sequencing reactions were performed as described above. Sequencing reactions were performed with amplicons generated with SEQ ID NOs.: 69 and 132 described above or SEQ ID NOs.: 69 and 118. Different sets of sequencing primers were used for each *S. aureus* strain: 1) SEQ ID NOs.: 69, 96, 117, 118, 120, 151, 152 for strains CCRI-9504, CCRI-2025, CCRI-1331, CCRI-9770 and CCRI-1377; 2) SEQ ID NOs.: 69, 96, 118 and 120 for strains CCRI-9208, CCRI-9681 and CCRI-9589; 3) SEQ ID NOs.: 69, 96, 117, 118, 120 and 152 for strain CCRI-9860; and 4) SEQ ID NOs.: 96, 117, 118, 119, 120, 151 and 152 for strain CCRI-9583.

The sequences obtained for 16 of the 20 strains non-amplifiable by the Hiramatsu assay (Table 4) were then compared to the sequences available from public databases. In all cases, portions of the sequence had an identity close to 100% to publicly available sequences for *orfX* (SEQ ID NOs.: 42-51, 165-168 and 171) or *mecA* and downstream region (SEQ ID NOs.: 27-31, 189-193, 195, 197-199 and 225). However, while the *orfX* portion of the fragments (SEQ ID NOs.: 42-51, 165-168 and 171) shared nearly 100% identity with the *orfX* gene of MSSA strain

NCTC 8325 described by Hiramatsu *et al.* (SEQ ID NO.: 3), the DNA sequence within the right extremity of SCC*mec* itself was shown to be very different from those of types I, II, III and IV described by Hiramatsu *et al.* (Table 13, Figure 4). Six different novel sequence types were obtained.

It should be noted that Hiramatsu *et al.* demonstrated that SCC*mec* type I could be associated with MREP type i, SCC*mec* types II and IV are associated with MREP type ii, and SCC*mec* type III is associated with MREP type iii. Our MREJ sequencing data from various MRSA strains led to the discovery of 6 novel MREP types designated types iv, v vi, vii, viii, and ix. The MREJ comprising distinct MREP types were named according to the MREP numbering scheme. Hence, MREP type i is comprised within MREJ type i, MREP type ii is comprised within MREJ type ii and so on up to MREP type ix.

The sequences within the right extremity of SCC*mec* obtained from strains CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504 (SEQ ID NOs.: 42, 43, 44, 45, 46 and 51) were nearly identical to each other and exhibited nearly 100% identity with IS*431* (GenBank accession numbers AF422691, ABO37671, AF411934). However, our sequence data revealed for the first time the location of this IS*431* sequence at the right extremity of SCC*mec* adjacent to the integration site. Therefore, as the sequences at the right extremity of SCC*mec* from these 6 MRSA strains were different from those of SCC*mec* type I from strain NCTC 10442, SCC*mec* type II from strain N315, SCC*mec* type III from strain 85/2082 and SCC*mec* type IV from strains CA05 and 8/6-3P described by Hiramatsu *et al.* (Ito *et al.,* 2001, Antimicrob. Agents Chemother. **45:**1323-1336; Ma *et al.,* 2002, Antimicrob. Agents Chemother. **46:**1147-1152), these new sequences were designated as MREP type iv (SEQ ID NOs.: 42-46 and 51). A BLAST search with the SCC*mec* portion of MREP type iv sequences produced significant alignments with sequences coding for portions of a variety of known

transposases. For example, when compared to Genbank accession no. AB037671, MREP type iv from SEQ ID NO. 51 shared 98% identity with the putative transposase of IS*431* and its downstream region; two gaps of 7 nucleotides each were also present in the alignment.

Sequences obtained from strains CCRI-1263, CCRI-1377, CCRI-1311 and CCRI-2025 (SEQ ID NOs.: 47-50) were nearly identical to each other and different from all three SCC*mec* types and MREP type iv and, consequently, were designated as MREP type v. When compared with Genbank sequences using BLAST, MREP type v sequences did not share any significant homology with any published sequence, except for the first 28 nucleotides. That short stretch corresponded to the last 11 coding nucleotides of *orfX*, followed by the 17 nucleotides downstream, including the right inverted repeat (IR-R) of SCC*mec*.

Sequence obtained from strain CCRI-9208 was also different from all three SCC*mec* types and MREP types iv and v and, consequently, was designated as MREP type vi (SEQ ID NO.: 171). Upon a BLAST search, MREP type vi was shown to be unique, exhibiting no significant homology to any published sequence.

Sequences obtained from strains CCRI-9583 and CCRI-9589 were also different from all three SCC*mec* types and MREP types iv to vi and were therefore designated as MREP type vii (SEQ ID NOs.: 165 and 166). Upon a BLAST search, MREP type vii was also shown to be unique, exhibiting no significant homology to any published sequence.

Sequence obtained from strain CCRI-9860 was also different from all three SCC*mec* types and MREP types iv to vii and was therefore designated as MREP type viii (SEQ ID NO.: 167). Sequence obtained from strain CCRI-9681 was also different from all three SCC*mec* types and MREP types iv to viii and was therefore designated as MREP type ix (SEQ ID NO.: 168). BLAST searches with the SCC*mec* portion of MREP types viii and ix sequences yielded significant alignments, but only for the first ~150 nucleotides of each MREP type. For

example, the beginning of the MREP type viii sequence had 88% identity with a portion of Genbank accession no. AB063173, but no significant homology with any published sequence was found for the rest of the sequence. In the same manner, the first ~150 nucleotides of MREP type ix had 97% identity with the same portion of AB063173, with the rest of the sequence being unique. The short homologous portion of MREP types viii and ix corresponds in AB063173 to the last 14 coding nucleotides of *orfX*, the IR-R of SCC*mec*, and a portion of *orf*CM009. Although sharing resemblances, MREP types viii and ix are very different from one another; as shown in Table 13, there is only 55.2% identity between both types for the first 500 nucleotides of the SCC*mec* portion.

Finally, we did not obtain any sequence within SSC*mec* from strain CCRI-9770. However, as described in the section "Sequencing of MREJ nucleotide sequences from MRSA strains not amplifiable with primers specific to SCC*mec* types I, II and III", this strain has apparently a partial or total deletion of the *orfX* and *orf*SA0022 genes in the chromosomal DNA to the right of the SCC*mec* integration site and this would represent a new right extremity junction. We therefore designated this novel sequence as MREP type x (SEQ ID NO.: 172). Future sequencing should reveal whether this so called MREJ type x contains a novel MREP type x or if the lack of amplification is indeed caused by variation in the chromosomal part of the MREJ.

The sequences of the first 500-nucleotide portion of the right extremity of all SCC*mec* obtained in the present invention were compared to those of SCC*mec* types I, II and III using GCG programs Pileup and Gap. Table 13 depicts the identities at the nucleotide level between SCC*mec* right extremities of the six novel sequences with those of SCC*mec* types I, II and III using the GCG program Gap. While SCC*mec* types I and II showed nearly 79.2% identity (differing only by a 102 bp insertion present in SCC*mec* type II) (Figures 1, 2 and 4), all other MREP types showed identities varying from 40.9 to 57.1%. This explains why the right

extremities of the novel MREP types iv to ix disclosed in the present invention could not have been predicted nor detected with the system described by Hiramatsu *et al.*

Four strains (CCRI-1312, CCRI-1325, CCRI-9773 and CCRI-9774) described in Table 3 were not sequenced but rather characterized using PCR primers. Strains CCRI-1312 and CCRI-1325 were shown to contain MREP type v using specific amplification primers described in Examples 4, 5 and 6 while strains CCRI-9773 and CCRI-9774 were shown to contain MREP type vii using specific amplification primers described in Example 7.

To obtain the complete sequence of the SCC*mec* present in the MRSA strains described in the present invention, primers targeting the*S. aureus* chromosome to the left (upstream of the *mecA* gene) of the SCC*mec* integration site were developed. Based on available public database sequences, 5 different primers were designed (SEQ ID NOs.: 85-89) (Table 9). These primers can be used in combination with *S. aureus* chromosome-specific primers in order to sequence the entire SCC*mec* or, alternatively, used in combination with a*mecA*-specific primer (SEQ ID NO.: 81) in order to sequence the left extremity junction ofSCC*mec*. We have also developed several primers specific to knownSCC*mec* sequences spread along the locus in order to obtain the complete sequence ofSCC*mec* (Table 9). These primers will allow to assign aSCC*mec* type to the MRSA strains described in the present invention.

Selection of amplification primers from SCC*mec/orfX* sequences

The MREJ sequences determined by the inventors or selected from public databases were used to select PCR primers for detection and identification of

MRSA. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various MREJ sequences.

Upon analysis of the six new MREP types iv to ixsequence data described above, primers specific to each new MREP type sequence (SEQ ID NOs.: 79, 80, 109, 112, 113, 115, 116 and 204) were designed (Figure 2, Table 5, Examples 3, 4, 5, 6, 7 and 8). Primers specific to MREP types iv, v and vii (SEQ IDNOs.: 79 , 80 and 112) were used in multiplex with the three primers to detect SCC*mec* types I, II and III (SEQ ID NOs: 64, 66 and 67) and the primer specific to the *S. aureus orfX* (SEQ ID NO. 64) (Examples 3, 4, 5, 6 and 7). Primers specific to MREP types vi, viii and ix (SEQ ID NOs.: 204, 115, 116 and 109) were also designed and tested against their specific target (Example 8).

Detection of amplification products

Classically, the detection of PCR amplification products is performed by standard ethidium bromide-stained agarose gel electrophoresis as described above. It is however clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Examples of such methods are described in co-pending patent application WO01/23604 A2.

Amplicon detection may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any sequence from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, amplicons can be characterized by sequencing. See co-pending patent application WO01/23604 A2 for examples of detection and sequencing methods.

In order to improve nucleic acid amplification efficiency, the composition of the reaction mixture may be modified (Chakrabarti and Schutt, 2002, Biotechniques, **32**:866-874; Al-Soud and Radstrom, 2002, J. Clin. Microbiol., **38**:4463-4470; Al-Soud and Radstrom, 1998, Appl. Environ. Microbiol., **64**:3748-3753; Wilson, 1997, Appl. Environ. Microbiol., **63**:3741-3751). Such modifications of the amplification reaction mixture include the use of various polymerases or the addition of nucleic acid amplification facilitators such asbetaine, BSA, sulfoxides, protein gp32, detergents, cations, tetramethylamonium chloride and others.

In a preferred embodiment, real-time detection of PCR amplification was monitored using molecular beacon probes in a SmartCycler® apparatus (Cepheid, Sunnyvale, CA). A multiplex PCR assay containing primers specific to MREP types i to v and *orfX* of *S. aureus* (SEQ ID NOs.: 64, 66, 67, 79 and 80), a molecular beacon probe specific to the *orfX* sequence (SEQ ID NO. 84, see Annex II and Figure 2) and an internal control to monitor PCR inhibition was developed. The internal control contains sequences complementary to MREP type iv- and *orfX*-specific primers (SEQ ID NOs. 79 and and 64). The assay also contains a molecular beacon probe labeled with tetrachloro-6-carboxyfluorescein (TET) specific to sequence within DNA fragment generated during amplification of the internal control. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM $MgCl_2$, 0.8 µM of each of the MREP-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of the MREP-specific primers (SEQ ID NOs.: 79 and 80), 80 copies of the internal control, 0.2 µM of the TET-labeled molecular beacon probe specific to the internal control, 0.2 µM of the molecular beacon probe (SEQ ID NO.: 84) labeled with 6-carboxyfluorescein (FAM), 330 µM of each of the four dNTPs (Pharmacia Biotech), 3.45 µg/µl of BSA (Sigma), and 0.875 U *Taq* polymerase (Promega) coupled with *Taq*Start™ Antibody (BD Biosciences). The PCR

amplification on the Smart Cycler® was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. Sensitivity tests performed by using purified genomic DNA from one MRSA strain of each MREP type (i to v) showed a detection limit of 2 to 10 genome copies (Example 5). None of the 26 MRCNS or 10 MSCNS tested were positive with this multiplex assay. The eight MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860, CCRI-9583, CCRI-9773, CCRI-9774, CCRI-9589) which harbor the new MREP types vi, viii, ix and x sequences described in the present invention remained undetectable (Example 5).

In a preferred embodiment, detection of MRSA using the real-time multiplex PCR assay on the Smart Cycler® apparatus (Cepheid, Sunnyvale, CA) directly from clinical specimens was evaluated. A total of 142 nasal swabs were collected during a MRSA hospital surveillance program at the Montreal General Hospital (Montreal, Quebec, Canada). The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, the swabs were plated onto mannitol agar and then the nasal material from the same swab was prepared with a simple and rapid specimen preparation protocol described in co-pending patent application number US 60/306,163. Classical identification of MRSA was performed by standard culture methods.

The PCR assay detected 33 of the 34 samples positive for MRSA based on the culture method. As compared to culture, the PCR assay detected 8 additional MRSA positive specimens for a sensitivity of 97.1 % and a specificity of 92.6 % (Example 6). This multiplex PCR assay represents a rapid and powerful method for the specific detection of MRSA carriers directly from nasal specimens and can be used with any types of clinical specimens such as wounds, blood or blood culture, CSF, etc.

In a preferred embodiement, a multiplex PCR assay containing primers specific to MREP types i, ii, iii, iv, v and vi and orfX of S. aureus (SEQ ID NOs.: 66, 67, 79, 80 and 112), and three molecular beacons probes specific to orfX sequence which allowed detection of the two sequence polymorphisms identified in this region of the orfX sequence was developed. Four of the strains which were not detected with the multiplex assay for the detection of MREP types i to v were now detected with this multiplex assay while the four MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860) which harbor the MREP types vi, viii, ix and x described in the present invention remained undetectable (Example 7). Primers soecific to MREP types vi, viii and ix (SEQ ID NOs.: 204, 115, 116 and 109) were also designed and were shown to detect their specific target strains (Example 8). While the primers and probes derived from the teaching of Hiramatsu *et al.*, permitted the detection of only 48.7% (19 strains out of 39) of the MRSA strains of Table 2, the primers and probes derived from the present invention enable the detection of 97.4 % of the strains (38 strains out of 39) (see exemples 7 and 8). Therefore it can be said that our assay has a ubiquity superior to 50% for the MRSA strains listed in Table 2.

Specificity, ubiquity and sensitivity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with staphylococcal species. All of the staphylococcal species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from microbial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Qbiogene, Carlsbad, CA) was used. Subsequently, the DNA was subjected to

amplification with the set of primers. Specific primers or probes hybridized only to the target DNA.

Oligonucleotides primers found to amplify specifically DNA from the target MRSA were subsequently tested for their ubiquity by amplification (i.e. ubiquitous primers amplified efficiently most or all isolates of MRSA). Finally, the analytical sensitivity of the PCR assays was determined by using 10-fold or 2-fold dilutions of purified genomic DNA from the targeted microorganisms. For most assays, sensitivity levels in the range of 2-10 genome copies were obtained. The specificity, ubiquity and analytical sensitivity of the PCR assays were tested either directly with bacterial cultures or with purified bacterial genomic DNA.

Molecular beacon probes were tested using the Smart Cycler® platform as described above. A molecular beacon probe was considered specific only when it hybridized solely to DNA amplified from the MREJ of *S. aureus*. Molecular beacon probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes detected efficiently most or all isolates of the MRSA) by hybridization to bacterial DNAs from various MRSA strains.

Bacterial strains

The reference strains used to build proprietary *SCCmec*-chromosome right extremity junction sequence data subrepertories, as well as to test the amplification and hybridization assays, were obtained from (i) the American Type Culture Collection (ATCC), (ii) the Laboratoire de santé publique du Québec (LSPQ) (Ste-Anne de Bellevue, Québec, Canada), (iii) the Centers for Disease Control and Prevention (CDC) (Atlanta, GA), (iv) the Institut Pasteur (Paris, France), and V) the Harmony Collection (London, United Kingdom) (Table 14). Clinical isolates of MRSA, MSSA, MRCNS and MSCNS from various geographical areas were also

used in this invention (Table 15). The identity of our MRSA strains was confirmed by phenotypic testing and reconfirmed by PCR analysis using *S. aureus*-specific primers and *mecA*-specific primers (SEQ ID NOs.: 69 and 81) (Martineau *et al.*, 2000, Antimicrob. Agents Chemother. **44**:231-238).

For sake of clarity, below is a list of the Examples, Tables, Figures and Annexes of this invention.

DESCRIPTION OF THE EXAMPLES

Example 1: Primers developed by Hiramatsu *et al.* can only detect MRSA strains belonging to MREP types i, ii, and iii while missing prevalent novel MREP types.

Example 2: Detection and identification of MRSA using primers specific to MREP types i, ii and iii sequences developed in the present invention.

Example 3: Development of a multiplex PCR assay on a standard thermocycler for detection and identification of MRSA based on MREP typesi, ii, iii, iv and v sequences.

Example 4: Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP typesi, ii, iii, iv and v sequences.

Example 5: Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP typesi, ii, iii, iv and v sequences and including an internal control.

Example 6: Detection of MRSA using the real-time multiplex assay on the Smart Cycler® based on MREP types i, ii, iii, iv and v sequences for the detection of MRSA directly from clinical specimens.

Example 7: Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP typesi, ii, iii, iv, v, vi and vii sequences.

Example 8: Developement of real-time PCR assays on the Smart Cycler® for detection and identification of MRSA based on MREP types vi, viii and ix.

DESCRIPTION OF THE TABLES

Table 1 provides information about all PCR primers developed byHiramatsu *et al.* in US patent 6,156,507.

Table 2 is a compilation of results (ubiquity and specificity) for the detection of SCC*mec-orfX* right extremity junction using primers described byHiramatsu *et al.* in US patent 6,156,507 on a standard thermocycler.

Table 3 is a list of MRSA strains notamplifiable using primers targeting types I, II and III of SCC*mec-orfX* right extremity junction sequences.

Table 4 is a list of novel sequences revealed in the present invention.

Table 5 provides information about all primers developed in the present invention.

Table 6 is a list of molecular beacon probes developed in the present invention.

Table 7 shows amplicon sizes of the different primer pairs described byHiramatsu *et al.* in US patent patent 6,156,507 or developed in the present invention.

Table 8 provides information about primers developed in the present invention to seequence the SCC*mec*-chromosome right extremity junction.

Table 9 provides information about primers developed in the present invention to obtain sequence of the complete SCC*mec*.

Table 10 is a list of the sequences available from public databases (GenBank, genome projects or US patent 6,156,507) used in the present invention to design primers and probes.

Table 11 gives analytical sensitivity of the PCR assay developed in the present invention using primers targeting types I, II and III ofSCC*me-orfX* right extremity junction sequences and performed using a standard thermocycler.

Table 12 is a compilation of results (ubiquity and specificity) for the detection of MRSA using primers developed in the present invention which target types I, II

and III of SCC*mec-orfX* right extremity junction sequences and performed using a standard thermocycler.

Table 13 shows a comparison of sequence identities between the first 500 nucleotides of SCC*mec* right extremities between 9 types of MREP.

Table 14 provides information about the reference strains of MRSA, MSSA, MRCNS and MSCNS used to validate the PCR assays developed in the present invention.

Table 15 provides information about the origin of clinical strains of MRSA, MSSA, MRCNS and MSCNS used to validate the PCR assays described in the present invention.

Table 16 depicts the analytical sensitivity of the PCR assay developed in the present invention using primers targeting 5 types of MREP sequences and performed on a standard thermocycler.

Table 17 is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers targeting 5 types of MREP sequences and performed on a standard thermocycler.

Table 18 depicts the analytical sensitivity of the PCR assay developed in the present invention using the SmartCycler® platform for the detection of 5 types of MREP.

Table 19 is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers and a molecular beacon probe targeting 5 types of MREP sequences and performed on the Smart Cycler® platform.

Table 20 depicts the analytical sensitivity of the PCR assay developed in the present invention using the SmartCycler® platform for the detection of 6 MREP types.

Table 21 is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers and a molecular beacon probe

targeting 6 types of MREP sequences and performed on the Smart Cycler® platform.

DESCRIPTION OF THE FIGURES

Figure 1 is a diagram illustrating the position of the primers developed by Hiramatsu *et al.* (US patent 6,156,507) in the SCC*mec*-chromosome right extremity junction for detection and identification of MRSA.

Figure 2 is a diagram illustrating the position of the primers selected in the present invention in the SCC*mec-orfX* right extremity junction for detection and identification of MRSA.

Figure 3 is a diagram illustrating the position of the primers selected in the present invention to sequence new MREP types.

Figure 4 illustrates a sequence alignment of nine MREP types.

FIGURE LEGENDS

Figure 1. Schematic organization of types I, II and III SCC*mecorfX* right extremity junctions and localization of the primers (SEQ ID NOs: 52-63) described by Hiramatsu *et al.* for the detection and identification of MRSA. Amplicon sizes are depicted in Table 7.

Figure 2. Schematic organization of MREP types i, ii, iii, iv, v, vi, vii, viii and ix and localization of the primers and molecular beacon targeting all MREP types (SEQ ID NOs. 20, 64, 66, 67, 79, 80, 84, 112, 115, 116, 84, 163 and 164) which were developed in the present invention. Amplicon sizes are depicted in Table 7.

Figure 3. Schematic organization of the SCC*mec*-chromosome right extremity junctions and localization of the primers (SEQ IDNOs. 65, 68, 69, 70, 77, 96, 118, 126, 132, 150 and 158) developed in the present invention for the sequencing of MREP types iv, v, vi, vii, viii, ix and x.

Figure 4. Multiple sequence alignment of representatives of nine MREP types (represented by portions of SEQ IDNOs.: 1, 2, 104, 51, 50, 171, 165, 167 and 168 for types i, ii, iii, iv, v, vi, vii, viii and ix, respectively).

DESCRIPTION OF THE ANNEXES

The Annexes show the strategies used for the selection of primers and internal probes:

Annex I illustrates the strategy for the selection of primers fromSCC*mec* and *orfX* sequences specific for SCC*mec* types I and II.

Annex II illustrates the strategy for the selection of specific molecular beacon probes for the real-time detection of SCC*mec-orfX* right extremity junctions.

As shown in these Annexes, the selected amplification primers may contain inosines and/or base ambiguities. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches were used. The inclusion of inosine and/or of degeneracies in the amplification primers allows mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach andDveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

EXAMPLES

EXAMPLE 1:

Primers developed by Hiramatsu *et al.* can only detect MRSA strains belonging to MREP types i, ii, and iii while missing prevalent novel MREP types.

As shown in Figure 1, Hiramatsu *et al.* have developed various primers that can specifically hybridize to the right extremities of types I, II and IIISCC*mec* DNAs. They combined these primers with primers specific to the *S. aureus* chromosome region located to the right of the SCC*mec* integration site for the detection of MRSA. The primer set (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) was shown by Hiramatsu *et al.* to be the most specific and ubiquitous for detection of MRSA. This set of primers gives amplification products of 1.5 kb for SCC*mec* type I, 1.6 kb for SCC*mec* type II and 1.0 kb for SCC*mec* type III (Table 7). The ubiquity and specificity of this multiplex PCR assay was tested on 39 MRSA strains, 41 MSSA strains, 9 MRCNS strains and 11 MSCNS strains (Table 2). One µL of a treated standardized bacterial suspension or of a bacterial genomic DNA preparation purified from bacteria were amplified in a 20 µl PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.4 µM of each of the SCC*mec*- and *orfX*-specific primers (SEQ ID NOs.: 56, 58 and 60), 200 µM of each of the four dNTPs (Pharmacia Biotech), 3.3 µg/µl of BSA (Sigma), and 0.5 U *Taq* polymerase (Promega) coupled with *Taq*Start™ Antibody (BD Biosciences).

PCR reactions were then subjected to thermal cycling: 3 min at 94°C followed by 40 cycles of 60 seconds at 95°C for the denaturation step, 60 seconds at 55°C for the annealing step, and 60 seconds at 72°C for the extension step, then followed by a terminal extension of 7 minutes at 72°C using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide.

None of the MRCNS or MSCNS strains tested were detected with the set of primers detecting SCC*mec* types I, II and III. Twenty of the 39 MRSA strains tested were not detected with this multiplex PCR assay (Tables 2 and 3). One of these undetected MRSA strains corresponds to the highly epidemic MRSA Portuguese clone (strain CCRI-9504; De Lencastre *et al.,* 1994. Eur. J. Clin. Microbiol. Infect. Dis. 13:64-73) and another corresponds to the highly epidemic MRSA Canadian clone CMRSA1 (strain CCRI-9589; Simor *et al.* CCDR 1999, 25-12, june 15). These data demonstrate that the primer set developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) is not ubiquitous for the detection of MRSA and suggest that some MRSA strains have sequences at the SCCmec right extremity junction which are different from those identified by Hiramatsu *et al.* other types of SCC*mec* sequences or other sequences at the right extremity of SCC*mec* (MREP type) are found in MRSA. A limitation of this assay is the non-specific detection of 13 MSSA strains (Table 2).

EXAMPLE 2:

Detection and identification of MRSA using primers specific to MREP types i, ii and iii sequences developed in the present invention. Based on analysis of multiple sequence alignments of *orfX* and SCC*mec* sequences described by Hiramatsu *et al.* or available from GenBank, a set of primers (SEQ ID NOs: 64, 66, 67) capable of amplifying short segments of types I, II and III of SCC*mec-orfX* right extremity junctions from MRSA strains and discriminating from MRCNS (Annex I and Figure 2) were designed. The chosen set of primers gives amplification products of 176 bp for SCC*mec* type I, 278 pb for SCC*mec* type II and 223 bp for SCC*mec* type III and allows rapid PCR amplification. These primers were used in multiplex PCR to test their ubiquity and specificity using 208 MRSA strains, 252 MSSA strains, 41 MRCNS strains and 21 MRCNS strains

(Table 12). The PCR amplification and detection was performed as described in Example 1. PCR reactions were then subjected to thermal cycling (3 minutes at 94°C followed by 30 or 40 cycles of 1 second at 95°C for thedenaturation step and 30 seconds at 60°C for the annealing-extension step, and then followed by a terminal extension of 2 minutes at 72°C) using a standardthermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made as described in Example1.

None of the MRCNS or MSCNS strains tested were detected with this set of primers (Table 12). However, the twenty MRSA strains which were not detected with the primer set developed by Hiramatsu *et al.* (SEQ ID NOs: 56, 58 and 60) were also not detected with the primers developed in the present invention (Tables 3 and 12). These data also demonstrate that some MRSA strains have sequences at the SCC*mec*-chromosome right extremity junction which are different from those identified by Hiramatsu *et al.* Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 12). The clinical significance of this finding remains to be established since these apparent MSSA strains could be the result of a recent deletion in the *mec* locus (Deplano *et al.*, 2000, J. Antimicrob. Chemotherapy, **46**:617-619; Inglis *et al.*, 1990, J. Gen. Microbiol., **136**:2231-2239; Inglis *et al.*, 1993, J. Infect. Dis., **167**:323-328; Lawrence *et al.* 1996, J. Hosp. Infect., **33**:49-53; Wada *et al.*, 1991, Biochem. Biophys. Res. Comm., **176**:1319-1326).

EXAMPLE 3:

Development of a multiplex PCR assay on a standard thermocycler for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences. Upon analysis of two of the new MREP types iv and v sequence data described in the present invention, two new primers (SEQ ID NOs.: 79 and 80)

were designed and used in multiplex with the three primers SEQ IDNOs.: 64, 66 and 67 described in Example 2. PCR amplification and detection of the PCR products was performed as described in Example 2. Sensitivity tests performed by using ten-fold or two-fold dilutions of purifiedgenomic DNA from various MRSA strains of each MREP type showed a detection limit of 5 to 10 genome copies (Table 16). Specificity tests were performed using 0,1 ng of purified genomic DNA or 1 µl of a standardized bacterial suspension. All MRCNS or MSCNS strains tested were negative with this multiplex assay (Table 17). Twelve of the 20 MRSA strains which were not detected with the multiplex PCR described in Examples 1 and 2 were now detected with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 12). The eight MRSA strains (CCRI-9208, CCRI-9583, CCRI-9773, CCRI-9774, CCRI-9589, CCRI-9860, CCRI-9681, CCRI-9770) and which harbor the new MREP types vi, vii, viii, ix and xsequences described in the present invention remained undetectable.

EXAMPLE 4:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences. The multiplex PCR assay described in Example 3 containing primers (SEQ ID NOs.: 64, 66, 67, 79 and 80) was adapted to the SmartCycler® platform (Cepheid). A molecular beacon probe specific to the *orfX* sequence was developed (SEQ ID NO. 84, see Annex II). Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.5 mM $MgCl_2$, 0.4 µM of each of the SCC*mec*- and *orfX*-specific primers (SEQ ID NOs.: 64, 66, 67, 79 and 80), 0.2 µM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 200 µM of each of the four dNTPs, 3.3 µg/µl of BSA, and 0.5 U *Taq* polymerase coupled with *Taq*Start™ Antibody. The PCR amplification onthe Smart Cycler® was performed

as follows: 3 min. at 94°C for initial denaturation, then forty-five cycles of three steps consisting of 5 seconds at 95°C for thedenaturation step, 15 seconds at 59°C for the annealing step and 10 seconds at 72°C for the extension step. Fluorescence detection was performed at the end of each annealing step. Sensitivity tests performed by using purified genomic DNA from several MRSA strains of each MREP type showed a detection limit of 2 to 10 genome copies (Table 18). None of the MRCNS or MSCNS were positive with this multiplex assay (Table 19). Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically. Twelve of the twenty MRSA strains which were not detected with the multiplex PCR described in Examples 1 and 2 were detected by this multiplex assay. As described in Example 3, the eight MRSA strains which harbor the new MREP types vi, vii, viii, ix and x sequences described in the present invention remained undetectable.

EXAMPLE 5:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences including an internal control. The multiplex PCR assay described in Example 4 containing primers specific to MREP typesi to v and *orfX* of *S. aureus* (SEQ ID NOs.: 64, 66, 67, 79 and 80) and a molecular beacon probe specific to the *orfX* sequence (SEQ ID NO. 84, see Annex II) was optimized to include an internal control to monitor PCR inhibition. This internal control contains sequences complementary to MREP type iv- and *orfX*-specific primers (SEQ ID NOs. 79 and and 64). The assay also contains a TET-labeled molecular beacon probe specific to sequence within the amplicon generated by amplification of the internal control. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM $MgCl_2$, 0.8 µM of each of the MREP-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of

the MREP-specific primers (SEQ ID NOs.: 79 and 80), 80 copies of the internal control, 0.2 μM of the TET-labeled molecular beacon probe specific to the internal control, 0.2 μM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 330 μM of each of the four dNTPs (Pharmacia Biotech), 3.45 μg/μl of BSA (Sigma), and 0.875 U *Taq* polymerase (Promega) coupled with *Taq*Start™ Antibody (BD Biosciences). The PCR amplification on the Smart Cycler® was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for thedenaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. Sensitivity tests performed by using purifiedgenomic DNA from one MRSA strain of each MREP type (i to v) showed a detection limit of 2 to 10 genome copies. None of the 26 MRCNS or 10 MSCNS were positive with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically. As described in Examples 3 and 4, the eight MRSA strains which harbor the new MREP types vi to x sequences described in the present invention remained undetectable.

EXAMPLE 6:

Detection of MRSA using the real-time multiplex assay on the SmartCycler® based on MREP types i, ii, iii, iv and v sequences directly from clinical specimens. The assay described in Example 5 was adapted for detection directly from clinical specimens. A total of 142 nasal swabs collected during a MRSA hospital surveillance program at the Montreal General Hospital (Montreal, Quebec, Canada) were tested. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, the swabs were plated onto mannitol agar and then the nasal material from the same swab was prepared with a simple and rapid specimen preparation protocol

described in co-pending patent application number US 60/306,163. Classical identification of MRSA was performed by standard culture methods.

The PCR assay described in Example 5 detected 33 of the 34 samples positive for MRSA based on the culture method. As compared to culture, the PCR assay detected 8 additional MRSA positive specimens for a sensitivity of 97.1 % and a specificity of 92.6 %. This multiplex PCR assay represents a rapid and powerful method for the specific detection of MRSA carriers directly from nasal specimens and can be used with any type of clinical specimens such as wounds, blood or blood culture, CSF, etc.

EXAMPLE 7:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv, v and vii sequences. Upon analysis of the new MREP type vii sequence data described in the present invention (SEQ ID NOs.:165 and 166), two new primers (SEQ ID NOs.: 112 and 113) were designed and tested in multiplex with the three primers SEQ ID NOs.: 64, 66 and 67 described in Example 2. Primer SEQ ID NO.: 112 was selected for use in the multiplex based on its sensitivity. Three molecular beacon probes specific to the *orfX* sequence which allowed detection of two sequence polymorphisms identified in this region of the *orfX* sequence, based on analysis of SEQ ID NOs.: 173-186, were also used in the multiplex (SEQ IDNOs.: 84, 163 and 164). Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM $MgCl_2$, 0.8 µM of each of the SCC*mec*-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of the SCC*mec*-specific primers (SEQ ID NOs.: 79 and 80), 0.2 µM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 330 µM of each of the four dNTPs (Pharmacia Biotech), 3.45 µg/µl of BSA (Sigma), and 0.875 U of

Taq polymerase (Promega) coupled with *Taq*Start™ Antibody (BD Biosciences). The PCR amplification on the Smart Cycler® was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. The detection of fluorescence was done at the end of each annealing step. Sensitivity tests performed by using purified genomic DNA from several MRSA strains of each MREP type showed a detection limit of 2 genome copies (Table 20). None of the 26 MRCNS or 8 MSCNS were positive with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 21). Four of the strains which were not detected with the multiplex assay for the detection of MREP types i to v were now detected with this multiplex assay while the four MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860) which harbor the MREP types vi, viii, ix and x described in the present invention remained undetectable.

EXAMPLE 8:

Developement of real-time PCR assays on the Smart Cycler® for detection and identification of MRSA based on MREP types vi, viii, ix. Upon analysis of the new MREP types vi, viii and ix sequence data described in the present invention, one new primers specific to MREP type vi (SEQ ID NO.: 201), one primer specific to MREP type viii (SEQ ID NO.: 115), a primer specific to MREP type ix (SEQ ID NO.: 109) and a primer specific to both MREP types viii and ix (SEQ ID NO.: 116) were designed. Each PCR primer was used in combination with the *orfX*-specific primer (SEQ ID NO.: 64) and tested against its specific target strain. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM $MgCl_2$, 0.4 µM of each of the SCC*mec*- and *orfX*-specific primers, 200 µM of each of the four dNTPs, 3.4 µg/µl of BSA, and 0.875

U *Taq* polymerase coupled with *Taq*Start™ Antibody. The PCR amplification was performed as described en Example 7. Sensitivity tests performed by using genomic DNA purified from their respective MRSA target strains showed that the best primer pair combination was SEQ ID NOs.: 64 and 115 for the detection of MREP types viii and ix simultaneously. These new SCC*mec*-specific primers may be used in multiplex with primers specific to MREP types i, ii, ii, iv, v and vii (SEQ ID NOs.: 64, 66, 67, 79 and 80) described in previous examples to provide a more ubiquitous MRSA assay.

In conclusion, we have improved the ubiquity of detection of MRSA strains. New MREJ types iv to x have been identified. Amongst strains representative of these new types, Hiramitsu's primers and/or probes succeeded in detecting less than 50% thereof. We have therefore amply passed the bar of at least 50% ubiquity, since our primers and probes were designed to detect 100% of the strains tested as representatives of MREJ types iv to ix. Therefore, although ubiquity depends on the pool of strains and representatives that are under analyse, we know now that close to 100% ubiquity is an attainable goal, when using the sequences of the right junctions (MREJ) to derive probes and primers dealing with polymorphism in this region. Depending on how many unknown types of MREJ exist, we have a margin of manoeuver going from 50% (higher than Hiramatsu's primers for the tested strains) to 100% if we sequence all the existing MREJs to derive properly the present diagnostic tools and methods, following the above teachings.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Table 1. PCR amplification primers reported by Hiramatsu *et al.* in US patent 6,156,507 found in the sequence listing

SEQ ID NO.: (present invention)	Target	Position[a,b]	SEQ ID NO.: (US pat. 6,156,507)
52	MREP types i and ii	480	18
53	MREP types i and ii	758	19
54	MREP types i and ii	927	20
55	MREP types i and ii	1154	21
56	MREP types i and ii	1755	22
57	MREP types i and ii	2302	23
58	MREP type iii	295[c]	24
59	*orfX*	1664	25
60	*orf*SA0022[d]	3267	28
61	*orf*SA0022[d]	3585	27
62	*orfX*	1389	26
63	*orf*SA0022[d]	2957	29

[a] Position refers to nucleotide position of the 5′ end of primer.

[b] Numbering for SEQ ID NOs.: 52-57 refers to SEQ ID NO.: 2; numbering for SEQ ID NO.: 58 refers to SEQ ID NO.: 4; numbering for SEQ ID NOs.: 59-63 refers to SEQ ID NO.: 3.

[c] Primer is reverse-complement of target sequence.

[d] *orf*SA0022 refers to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 2. Specificity and ubiquity tests performed on a standard thermocycler using the optimal set of primers described by Hiramatsu *et al.* (SEQ ID NOs. : 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) for the detection of MRSA

Strains	PCR results for SCC*mec* - *orfX* right extremity junction	
	Positive (%)	Negative (%)
MRSA - 39 strains	19 (48.7)	20 (51.2)
MSSA - 41 strains	13 (31.7)	28 (68.3)
MRCNS - 9 strains*	0 (0%)	9 (100%)
MSCNS - 11 strains*	0 (0%)	11 (100%)

*** Details regarding CNS strains:**

MRCNS :
- *S. caprae* (1)
- *S. cohni cohnii* (1)
- *S. epidermidis* (1)
- *S. haemolyticus* (2)
- *S. hominis* (1)
- *S. sciuri* (1)
- *S. simulans* (1)
- *S. warneri* (1)

MSCNS :
- *S. cohni cohnii* (1)
- *S. epidermidis* (1)
- *S. equorum (1)*
- *S. gallinarum (1)*
- *S. haemolyticus* (1)
- *S. lentus* (1)
- *S. lugdunensis* (1)
- *S. saccharolyticus* (1)
- *S. saprophyticus* (2)
- *S. xylosus (1)*

Table 3. Origin of MRSA strains not amplifiable using primers developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) as well as primers developed in the present invention targeting MREP types i, ii and iii (SEQ ID NOs.: 64, 66 and 67)

Staphylococcus aureus strain designation: Original	CCRI[a]	Origin
ATCC BAA-40[b]	CCRI-9504	Portugal
ATCC 33592	CCRI-178	USA
R991282	CCRI-2025	Québec, Canada
4508	CCRI-9208	Québec, Canada
19121	CCRI-8895	Denmark
Z109	CCRI-8903	Denmark
45302	CCRI-1263	Ontario, Canada
R655	CCRI-1324	Québec, Canada
MA 50428	CCRI-1311	Québec, Canada
MA 50609	CCRI-1312	Québec, Canada
MA 51363	CCRI-1331	Québec, Canada
MA 51561	CCRI-1325	Québec, Canada
14A0116	CCRI-9681	Poland
23 (CCUG 41787)	CCRI-9860	Sweden
SE26-1	CCRI-9770	Ontario, Canada
SE1-1	CCRI-9583	Ontario, Canada
ID-61880[c]	CCRI-9589	Ontario, Canada
SE47-1	CCRI-9773	Ontario, Canada
SE49-1	CCRI-9774	Ontario, Canada
39795-2	CCRI-1377	Québec, Canada

[a] CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

[b] Portuguese clone.

[c] Canadian clone EMRSA1.

Table 4. *Staphylococcus aureus* MREJ nucleotide sequences revealed in the present invention

SEQ ID NO.	*Staphylococcus aureus* strain designation: Original	CCRI[a]	Genetic Target
27	R991282	CCRI-2025	*mecA*
28	45302	CCRI-1263	*mecA*
29	MA 50428	CCRI-1311	*mecA*
30	MA 51363	CCRI-1331	*mecA*
31	39795-2	CCRI-1377	*mecA* and 1.5 kb of downstream region
42	ATCC 33592	CCRI-178	MREP type iv
43	19121	CCRI-8895	MREP type iv
44	Z109	CCRI-8903	MREP type iv
45	R655	CCRI-1324	MREP type iv
46	MA 51363	CCRI-1331	MREP type iv
47	45302	CCRI-1263	MREP type v
48	39795-2	CCRI-1377	MREP type v
49	MA 50428	CCRI-1311	MREP type v
50	R991282	CCRI-2025	MREP type v
51	ATCC BAA-40	CCRI-9504	MREP type iv
165	SE1-1	CCRI-9583	MREP type vii
166	ID-61880	CCRI-9589	MREP type vii
167	23 (CCUG 41787)	CCRI-9860	MREP type viii
168	14A016	CCRI-9681	MREP type ix
171	4508	CCRI-9208	MREP type vi
172	SE26-1	CCRI-9770	*orf*SA0021[b] and 75 bp of *orf*SA0022[b]
173	26 (98/10618)	CCRI-9864	MREP type ii
174	27 (98/26821)	CCRI-9865	MREP type ii
175	28 (24344)	CCRI-9866	MREP type ii
176	12 (62305)	CCRI-9867	MREP type ii
177	22 (90/14719)	CCRI-9868	MREP type ii
178	23 (98/14719)	CCRI-9869	MREP type ii
179	32 (97S99)	CCRI-9871	MREP type ii
180	33 (97S100)	CCRI-9872	MREP type ii
181	38 (825/96)	CCRI-9873	MREP type ii
182	39 (842/96)	CCRI-9874	MREP type ii
183	43 (N8-892/99)	CCRI-9875	MREP type ii
184	46 (9805-0137)	CCRI-9876	MREP type iii
185	1	CCRI-9882	MREP type ii
186	29	CCRI-9885	MREP type ii
189	SE1-1	CCRI-9583	*mecA* and 2.2 kb of downstream region, including IS*431mec*
190	ATCC BAA-40	CCRI-9504	*mecA* and 1.5 kb of downstream region
191	4508	CCRI-9208	*mecA* and 0.9 kb of downstream region
192	ID-61880	CCRI-9589	*mecA* and 0.9 kb of downstream region
193	14A016	CCRI-9681	*mecA* and 0.9 kb of downstream region
195	SE26-1	CCRI-9770	*mecA* and 1.5 kb of downstream region, including IS*431mec*
197	ATCC 43300	CCRI-175	MREP type ii
198	R522	CCRI-1262	MREP type iii
199	13370	CCRI-8894	MREP type i
219	ATCC BAA-40	CCRI-9504	*tetK*

Table 4. *Staphylococcus aureus* MREJ nucleotide sequences revealed in the present invention (continued)

SEQ ID NO.	*Staphylococcus aureus* strain designation: Original	CCRI[b]	Genetic Target[a]
220	MA 51363	CCRI-1331	*mecA* and 1.5 kb of downstream region
221	39795-2	CCRI-1377	IS*431mec* and 0.6 kb of upstream region
222	R991282	CCRI-2025	*mecA* and 1.5 kb of downstream region
223	R991282	CCRI-2025	IS*431mec* and 0.6 kb of upstream region
224	23 (CCUG 41787)	CCRI-9860	*mecA* and 1.5 kb of downstream region
225	23 (CCUG 41787)	CCRI-9860	IS*431mec* and 0.6 kb of upstream region
233	14A016	CCRI-9681	MREP type ix

[a] CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

[b] *orfSA0021* and *orfSA0022* refer to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 5. PCR primers developed in the present invention

SEQ ID NO.	Target	Originating DNA Position[a]	Originating DNA SEQ ID NO.
64	*orfX*	1720	3
70	*orfX*	1796	3
71	*orfX*	1712	3
72	*orfX*	1749	3
73	*orfX*	1758	3
74	*orfX*	1794	3
75	*orfX*	1797	3
76	*orfX*	1798	3
66	MREP types i and ii	2327	2
100	MREP types i and ii	2323	2
101	MREP types i and ii	2314	2
97	MREP type ii	2434	2
99	MREP type ii	2434	2
67	MREP type iii	207[b]	4
98	MREP type iii	147[b]	4
102	MREP type iii	251[b]	4
79	MREP type iv	74[b]	43
80	MREP type v	50[b]	47
109	MREP type ix	652[b]	168
204	MREP type vi	642[b]	171
112	MREP type vii	503[b]	165
113	MREP type vii	551[b]	165
115	MREP type viii	514[b]	167
116	MREP type viii	601[b]	167

[a] Position refers to nucleotide position of 5' end of primer.

[b] Primer is reverse-complement of target sequence.

Table 6. Molecular beacon probes developed in the present invention

SEQ ID NO.	Target	Position
32	*orfX*	86[a]
83	*orfX*	86[a]
84	*orfX*	34[a,b]
160	*orfX*	55[a,b]
161	*orfX*	34[a,b]
162	*orfX*	114[a]
163	*orfX*	34[a,b]
164	*orfX*	34[a,b]

[a] Position refers to nucleotide position of the 5′ end of the molecular beacon's loop on SEQ ID NO.: 3.

[b] Sequence of molecular beacon's loop is reverse-complement of SEQ ID NO.: 3.

Table 7. Length of amplicons obtained with the different primer pairs which are objects of the present invention

SEQ ID NO.	Target[d]	Amplicon length[a]
59/52[b]	*orfX*/MREP type i and ii	2079 (type i);2181 (type ii)
59/53[b]	*orfX*/MREP type i and ii	1801 (type i);1903 (type ii)
59/54[b]	*orfX*/MREP type i and ii	1632 (type i);1734 (type ii)
59/55[b]	*orfX*/MREP type i and ii	1405 (type i);1507 (type ii)
59/56[b]	*orfX*/MREP type i and ii	804 (type i);906 (type ii)
59/57[b]	*orfX*/MREP type i and ii	257 (type i);359 (type ii)
60/52[b]	*orf*SA0022/MREP type i and ii	2794 (type i);2896 (type ii)
60/53[b]	*orf*SA0022/MREP type i and ii	2516 (type i);2618 (type ii)
60/54[b]	*orf*SA0022/MREP type i and ii	2347 (type i);2449 (type ii)
60/55[b]	*orf*SA0022/MREP type i and ii	2120 (type i);2222 (type ii)
60/56[b]	*orf*SA0022/MREP type i and ii	1519 (type i);1621 (type ii)
60/57[b]	*orf*SA0022/MREP type i and ii	972 (type i);1074 (type ii)
61/52[b]	*orf*SA0022/MREP type i and ii	2476 (type i);2578 (type ii)
61/53[b]	*orf*SA0022/MREP type i and ii	2198 (type i);2300 (type ii)
61/54[b]	*orf*SA0022/MREP type i and ii	2029 (type i);2131 (type ii)
61/55[b]	*orf*SA0022/MREP type i and ii	1802 (type i);1904 (type ii)
61/56[b]	*orf*SA0022/MREP type i and ii	1201 (type i);1303 (type ii)
61/57[b]	*orf*SA0022/MREP type i and ii	654 (type i);756(type ii)
62/52[b]	*orfX*/MREP type i and ii	2354 (type i);2456 (type ii)
62/53[b]	*orfX*/MREP type i and ii	2076 (type i);2178 (type ii)
62/54[b]	*orfX*/MREP type i and ii	1907 (type i);2009 (type ii)
62/55[b]	*orfX*/MREP type i and ii	1680 (type i);1782 (type ii)
62/56[b]	*orfX*/MREP type i and ii	1079 (type i);1181 (type ii)
62/57[b]	*orfX*/MREP type i and ii	532 (type i);634 (type ii)
63/52[b]	*orf*SA0022/MREP type i and ii	3104 (type i);3206 (type ii)
63/53[b]	*orf*SA0022/MREP type i and ii	2826 (type i);2928 (type ii)
63/54[b]	*orf*SA0022/MREP type i and ii	2657 (type i);2759 (type ii)
63/55[b]	*orf*SA0022/MREP type i and ii	2430 (type i);2532 (type ii)
63/56[b]	*orf*SA0022/MREP type i and ii	1829 (type i);1931 (type ii)
63/57[b]	*orf*SA0022/MREP type i and ii	1282 (type i);1384 (type ii)
59/58[b]	*orfX*/MREP type iii	361
60/58[b]	*orf*SA0022/MREP type iii	1076
61/58[b]	*orf*SA0022/MREP type iii	758
62/58[b]	*orfX*/MREP type iii	656
63/58[b]	*orf*SA0022/MREP type iii	1386
70/66	*orfX*/MREP type i and ii	100 (type i);202 (type ii)
70/67	*orfX*/MREP type iii	147 (type iii)
64/66[c]	*orfX*/MREP type i and ii	176 (type i);278 (type ii)
64/67[c]	*orfX*/MREP type iii	223
64/79[c]	*orfX*/MREP type iv	215
64/80[c]	*orfX*/MREP type v	196
64/97[c]	*orfX*/MREP type ii	171
64/98[c]	*orfX*/MREP type iii	163
64/99[c]	*orfX*/MREP type ii	171
64/100[c]	*orfX*/MREP types i and ii	180 (type i);282 (type ii)
64/101[c]	*orfX*/MREP types i and ii	189 (type i);291 (type ii)
64/102[c]	*orfX*/MREP type iii	263
64/109[c]	*orfX*/MREP type ix	369
64/204[c]	*orfX*/MREP type vi	348
64/112[c]	*orfX*/MREP type vii	214
64/113[c]	*orfX*/MREP type vii	263
64/115[c]	*orfX*/MREP type viii	227
64/116[c]	*orfX*/MREP type viii	318

[a] Amplicon length is given in base pairs for MREP types amplified by the set of primers.

[b] Set of primers described by Hiramatsu *et al.* in US patent 6,156,507.

[c] Set of primers developed in the present invention.

[d] *orf*SA0022 refers to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 8. Other primers developed in the present invention

SEQ ID NO.	Target	Originating DNA Position[a]	Originating DNA SEQ ID NO.
77	MREP type iv	993	43
65	MREP type v	636	47
70	*orfX*	1796	3
68	IS*431*	626	92
69	*mecA*	1059	78
96	*mecA*	1949	78
81	*mecA*	1206	78
114	MREP type vii	629[b]	165
117	MREP type ii	856	194
118	MREP type ii	974[b]	194
119	MREP type vii	404	189
120	MREP type vii	477[b]	189
123	MREP type vii	551	165
124	MREP type ii	584	170
125	MREP type ii	689[b]	170
126	*orf*SA0021	336	231
127	*orf*SA0021	563	231
128	*orf*SA0022[d]	2993	231
129	*orf*SA0022[d]	3467[b]	231
132	*orfX*	3700	231
145	MREP type iv	988	51
146	MREP type v	1386	51
147	MREP type iv	891[b]	51
148	MREP type ix	664	168
149	MREP type ix	849[b]	168
150	MREP type vii	1117[b]	165
151	MREP type vii	1473	189
152	IS*431mec*	1592[b]	189
154	MREP type v	996[b]	50
155	MREP type v	935	50
156	*tetK* from plasmid pT181	1169[b]	228
157	*tetK* from plasmid pT181	136	228
158	*orfX*	2714[b]	2
159	*orfX*	2539	2
187	MREP type viii	967[b]	167
188	MREP type viii	851	167

[a] Position refers to nucleotide position of the 5′ end of primer.

[b] Primer is reverse-complement of target sequence.

Table 9. Amplification and/or sequencing primers developed in the present invention

SEQ ID NO.	Target	Originating DNA Position[a]	Originating DNA SEQ ID NO.
85	*S. aureus* chromosome	197[b]	35
86	*S. aureus* chromosome	198[b]	37
87	*S. aureus* chromosome	197[b]	38
88	*S. aureus* chromosome	1265[b]	39
89	*S. aureus* chromosome	1892	3
103	*orfX*	1386	3
105	MREP type i	2335	2
106	MREP type ii	2437	2
107	MREP type iii	153[b]	4
108	MREP type iii	153[b]	4
121	MREP type vii	1150	165
122	MREP type vii	1241[b]	165
130	*orfX*	4029[b]	231
131	region between *orf*SA0022 and *orf*SA0023[d]	3588	231
133	*merB* from plasmid pI258	262	226
134	*merB* from plasmid pI258	539[b]	226
135	*merR* from plasmid pI258	564	226
136	*merR* from plasmid pI258	444	227
137	*merR* from plasmid pI258	529	227
138	*merR* from plasmid pI258	530[b]	227
139	*rep* from plasmid pUB110	796	230
140	*rep* from plasmid pUB110	761[b]	230
141	*rep* from plasmid pUB110	600	230
142	*aadD* from plasmid pUB110	1320[b]	229
143	*aadD* from plasmid pUB110	759	229
144	*aadD* from plasmid pUB110	646	229
153	MREP type vii	1030	165
200	*orf*SA0022[d]	871[c]	231
201	*orf*SA0022[d]	1006	231
202	MREP type vi	648	171
203	MREP type vi	883[b]	171
205	MREP type ix	1180	168
206	MREP type ix	1311[b]	233
207	MREP type viii	1337	167
208	MREP type viii	1441[b]	167
209	*ccrA*	184	232
210	*ccrA*	385	232
211	*ccrA*	643[b]	232
212	*ccrA*	1282[b]	232
213	*ccrB*	1388	232
214	*ccrB*	1601	232
215	*ccrB*	2139[b]	232
216	*ccrB*	2199[b]	232
217	*ccrB*	2847[b]	232
218	*ccrB*	2946[b]	232

[a] Position refers to nuclectide position of the 5′ end of primer.

[b] Primer is reverse-complement of target sequence.

[c] Primer contains two mismatches.

[d] *orf*SA0022 and *orf*SA0023 refer to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 10. Origin of the nucleic acids and/or sequences available from public databases found in the sequence listing

SEQ ID NO.	Staphylococcal strain	Source	Accession number	Genetic Target[a, b]
1	NCTC 10442	Database	AB033763	*SCCmec* type I MREJ
2	N315	Database	D86934	*SCCmec* type II MREJ
3	NCTC 8325	Database	AB014440	MSSA chromosome
4	86/560	Database	AB013471	*SCCmec* type III MREJ
5	86/961	Database	AB013472	*SCCmec* type III MREJ
6	85/3907	Database	AB013473	*SCCmec* type III MREJ
7	86/2652	Database	AB013474	*SCCmec* type III MREJ
8	86/1340	Database	AB013475	*SCCmec* type III MREJ
9	86/1762	Database	AB013476	*SCCmec* type III MREJ
10	86/2082	Database	AB013477	*SCCmec* type III MREJ
11	85/2111	Database	AB013478	*SCCmec* type III MREJ
12	85/5495	Database	AB013479	*SCCmec* type III MREJ
13	85/1836	Database	AB013480	*SCCmec* type III MREJ
14	85/2147	Database	AB013481	*SCCmec* type III MREJ
15	85/3619	Database	AB013482	*SCCmec* type III MREJ
16	85/3566	Database	AB013483	*SCCmec* type III MREJ
17	85/2232	Database	AB014402	*SCCmec* type II MREJ
18	85/2235	Database	AB014403	*SCCmec* type II MREJ
19	MR108	Database	AB014404	*SCCmec* type II MREJ
20	85/9302	Database	AB014430	*SCCmec* type I MREJ
21	85/9580	Database	AB014431	*SCCmec* type I MREJ
22	85/1940	Database	AB014432	*SCCmec* type I MREJ
23	85/6219	Database	AB014433	*SCCmec* type I MREJ
24	64/4176	Database	AB014434	*SCCmec* type I MREJ
25	64/3846	Database	AB014435	*SCCmec* type I MREJ
26	HUC19	Database	AF181950	*SCCmec* type II MREJ
33	G3	US 6,156,507	SEQ ID NO.: 15	*S. epidermidis* *SCCmec* type II MREJ
34	SH 518	US 6,156,507	SEQ ID NO.: 16	*S. haemolyticus* *SCCmec* type II MREJ
35	ATCC 25923	US 6,156,507	SEQ ID NO.: 9	*S. aureus* chromosome
36	STP23	US 6,156,507	SEQ ID NO.: 10	*S. aureus* chromosome
37	STP43	US 6,156,507	SEQ ID NO.: 12	*S. aureus* chromosome
38	STP53	US 6,156,507	SEQ ID NO.: 13	*S. aureus* chromosome
39	476	Genome project[c]		*S. aureus* chromosome
40	252	Genome project[c]		*SCCmec* type II MREJ
41	COL	Genome project[d]		*SCCmec* type I MREJ
78	NCTC 8325	Database	X52593	*mecA*
82	NCTC 10442	Database	AB033763	*mecA*
90	N315	Database	D86934	*mecA*
91	85/2082	Database	AB037671	*mecA*
92	NCTC 10442	Database	AB033763	*IS431*
93	N315	Database	D86934	*IS431*
94	HUC19	Database	AF181950	*IS431*
95	NCTC 8325	Database	X53818	*IS431*
104	85/2082	Database	AB037671	*SCCmec* type III MREJ
226	unknown	Database	L29436	*merB* on plasmid pI258
227	unknown	Database	L29436	*merR* on plasmid pI258
228	unknown	Database	S67449	*tetK* on plasmid pT181
229	HUC19	Database	AF181950	*aadD* on plasmid pUB110
230	HUC19	Database	AF181950	*rep* on plasmid pUB110
231	N315	Database	AP003129	*orfSA0021*, *orfSA0022*, *orfSA0023*
232	85/2082	Database	AB037671	*ccrA/ccrB*

[a] MREJ refers to *mec* right extremity junction and includes sequences from SCC*mec*-right extremity and chromosomal DNA to the right of SCC*mec* integration site.

[b] Unless otherwise specified, all sequences were obtained from *S. aureus* strains.

[c] Sanger Institute genome project (http://www.sanger.ac.uk).

[d] TIGR genome project (http://www.tigr.org).

Table 11. Analytical sensitivity of the MRSA-specific PCR assay targeting MREP types i, ii and iii on a standard thermocycler using the set of primers developed in the present invention (SEQ ID NOs.: 64, 66 and 67)

Strain designation : Original	CCRI[a] (MREP type)	Detection limit (number of genome copies)
13370	CCRI-8894 (I)	5
ATCC 43300	CCRI-175 (II)	2
35290	CCRI-1262 (III)	2

[a] CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 12. Specificity and ubiquity tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii and iii developed in the present invention (SEQ ID NOs.: 64, 66 and 67) for the detection of MRSA

Strains	PCR results for MREJ	
	Positive (%)	Negative (%)
MRSA - 208 strains	188 (90.4)	20 (9.6)
MSSA - 252 strains	13 (5.2)	239 (94.8)
MRCNS - 41 strains*	0	42 (100)
MSCNS - 21 strains*	0	21 (100)

*** Details regarding CNS strains:**

MRCNS :
- *S. caprae* (2)
- *S. cohni cohnii* (3)
- *S. cohni urealyticum* (4)
- *S. epidermidis* (8)
- *S. haemolyticus* (9)
- *S. hominis* (4)
- *S. sciuri* (4)
- *S. sciuri sciuri* (1)
- *S. simulans* (3)
- *S. warneri* (3)

MSCNS :
- *S. cohni cohnii* (1)
- *S. epidermidis* (3)
- *S. equorum* (2)
- *S. felis* (1)
- *S. gallinarum* (1)
- *S. haemolyticus* (1)
- *S. hominis* (1)
- *S. lentus* (1)
- *S. lugdunensis* (1)
- *S. saccharolyticus* (1)
- *S. saprophyticus* (5)
- *S. simulans* (1)
- *S. warneri* (1)
- *S. xylosus (1)*

Table 13. Percentage of sequence identity for the first 500 nucleotides of SCC*mec* right extremities between all 9 types of MREP[a,b]

MREP type	i	ii	iii	iv	v	vi	vii	viii	ix
i	--	79.2	42.8	42.8	41.2	44.4	44.6	42.3	42.1
ii			43.9	47.5	44.7	41.7	45.0	52.0	57.1
iii				46.8	44.5	42.9	45.0	42.8	45.2
iv					45.8	41.4	44.3	48.0	41.3
v						45.4	43.7	47.5	44.3
vi							45.1	41.1	47.2
vii								42.8	40.9
viii									55.2
ix									--

[a] "First 500 nucleotides" refers to the 500 nucleotides within the *SCCmec* right extremity, starting from the integration site of SCC*mec* in the *Staphylococcus aureus* chromosome as shown on Figure 4.

[b] Sequences were extracted from SEQ ID NOs.: 1, 2, 104, 51, 50, 171, 165, 167, and 168 for types i to ix, respectively.

Table 14. Reference strains used to test sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences

Staphylococcal species	Strains	Source[a]
MRSA (n = 45)	33591	ATCC
	33592	ATCC
	33593	ATCC
	BAA-38	ATCC
	BAA-39	ATCC
	BAA-40	ATCC
	BAA-41	ATCC
	BAA-42	ATCC
	BAA-43	ATCC
	BAA-44	ATCC
	F182	CDC
	23 (CCUG 41787)	HARMONY Collection
	ID-61880 (EMRSA1)	LSPQ
	MA 8628	LSPQ
	MA 50558	LSPQ
	MA 50428	LSPQ
	MA 50609	LSPQ
	MA 50884	LSPQ
	MA 50892	LSPQ
	MA 50934	LSPQ
	MA 51015	LSPQ
	MA 51056	LSPQ
	MA 51085	LSPQ
	MA 51172	LSPQ
	MA 51222	LSPQ
	MA 51363	LSPQ
	MA 51561	LSPQ
	MA 52034	LSPQ
	MA 52306	LSPQ
	MA 51520	LSPQ
	MA 51363	LSPQ
	98/10618	HARMONY Collection
	98/26821	HARMONY Collection
	24344	HARMONY Collection
	62305	HARMONY Collection
	90/10685	HARMONY Collection
	98/14719	HARMONY Collection
	97S99	HARMONY Collection
	97S100	HARMONY Collection
	825/96	HARMONY Collection
	842/96	HARMONY Collection
	N8-890/99	HARMONY Collection
	9805-01937	HARMONY Collection
	1	Kreiswirth-1
	29	Kreiswirth-1
MRCNS (n = 4)	29060	ATCC
	35983	ATCC
	35984	ATCC
	2514	LSPQ

Table 14. Reference strains used to test sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences (continued)

Staphylococcal species	Strains	Source
MSSA (n = 28)	MA 52263	LSPQ
	6538	ATCC
	13301	ATCC
	25923	ATCC
	27660	ATCC
	29213	ATCC
	29247	ATCC
	29737	ATCC
	RN 11	CDC
	RN 3944	CDC
	RN 2442	CDC
	7605060113	CDC
	BM 4611	Institut Pasteur
	BM 3093	Institut Pasteur
	3511	LSPQ
	MA 5091	LSPQ
	MA 8849	LSPQ
	MA 8871	LSPQ
	MA 50607	LSPQ
	MA 50612	LSPQ
	MA 50848	LSPQ
	MA 51237	LSPQ
	MA 51351	LSPQ
	MA 52303	LSPQ
	MA 51828	LSPQ
	MA 51891	LSPQ
	MA 51504	LSPQ
	MA 52535	LSPQ
	MA 52783	LSPQ
MSCNS (n = 17)	12228	ATCC
	14953	ATCC
	14990	ATCC
	15305	ATCC
	27836	ATCC
	27848	ATCC
	29070	ATCC
	29970	ATCC
	29974	ATCC
	35539	ATCC
	35552	ATCC
	35844	ATCC
	35982	ATCC
	43809	ATCC
	43867	ATCC
	43958	ATCC
	49168	ATCC

[a] ATCC stands for "American Type Culture Collection".
LSPQ stands for "Laboratoire de Santé Publique du Québec".
CDC stands for "Center for Disease Control and Prevention".

Table 15. Clinical isolates used to test the sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences

Staphylococcal species	Number of strains	Source
MRSA (n = 177)	150	Canada
	10	China
	10	Denmark
	9	Argentina
	1	Egypt
	1	Sweden
	1	Poland
	3	Japan
	1	France
MSSA (n = 224)	208	Canada
	10	China
	4	Japan
	1	USA
	1	Argentina
MRCNS (n = 38)	32	Canada
	3	China
	1	France
	1	Argentina
	1	USA
MSCNS (n = 17)	14	UK
	3	Canada

Table 16. Analytical sensitivity of tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NOs.: 64, 66, 67, 79 and 80) developed in the present invention for the detection and identification of MRSA

Staphylococcus aureus strain designation: Original	CCRI[a] (MREP type)	Detection limit (*number of genome copies*)
13370	CCRI-8894 (i)	10
ATCC 43300	CCRI-175 (ii)	5
9191	CCRI-2086 (ii)	10
35290	CCRI-1262 (iii)	5
352	CCRI-1266 (iii)	10
19121	CCRI-8895 (iv)	5
ATCC 33592	CCRI-178 (iv)	5
MA 50428	CCRI-1311 (v)	5
R991282	CCRI-2025 (v)	5

[a] CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 17. Specificity and ubiquity tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NO.: 64, 66, 67, 79 and 80) developed in the present invention for the detection and identification of MRSA

Strains	PCR results for SCC*mec* - *orfX* right extremity junction	
	Positive (%)	Negative (%)
MRSA - 35 strains[a]	27 (77.1)	8 (22.9)
MSSA - 44 strains	13 (29.5)	31 (70.5)
MRCNS - 9 strains[*]	0	9 (100)
MSCNS - 10 strains[*]	0	10 (100)

[a] MRSA strains include the 20 strains listed in Table 3.

[*]**Details regarding CNS strains:**

MRCNS : *S. caprae* (1)
S. cohni cohnii (1)
S. epidermidis (1)
S. haemolyticus (2)
S. hominis (1)
S. sciuri (1)
S. simulans (1)
S. warneri (1)

MSCNS : *S. cohni* (1)
S. epidermidis (1)
S. equorum (1)
S. haemolyticus (1)
S. lentus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
S. saprophyticus (2)
S. xylosus (1)

Table 18. Analytical sensitivity of tests performed on the Smart Cycler® thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NOs.: 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO.: 84) developed in the present invention for the detection and identification of MRSA

Staphylococcus aureus strain designation: Original	CCRI[a] (MREP type)	Detection limit (number of genome copies)
13370	CCRI-8894 (i)	2
ATCC 43300	CCRI-175 (ii)	2
9191	CCRI-2086 (ii)	10
35290	CCRI-1262 (iii)	2
352	CCRI-1266 (iii)	10
ATCC 33592	CCRI-178 (iv)	2
MA 51363	CCRI-1331(iv)	5
19121	CCRI-8895 (iv)	10
Z109	CCRI-8903 (iv)	5
45302	CCRI-1263 (v)	10
MA 50428	CCRI-1311 (v)	5
MA 50609	CCRI-1312 (v)	5
MA 51651	CCRI-1325 (v)	10
39795-2	CCRI-1377 (v)	10
R991282	CCRI-2025 (v)	2

[a] CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 19. Specificity and ubiquity tests performed on the Smart Cycler® thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NO. : 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO. : 84) developed in the present invention for the detection of MRSA

Strains	PCR results for MREJ	
	Positive (%)	Negative (%)
MRSA - 29 strains[a]	21 (72.4)	8 (27.6)
MSSA - 35 strains	13 (37.1)	22 (62.9)
MRCNS - 14 strains	0	14 (100)
MSCNS - 10 strains	0	10 (100)

[a] MRSA strains include the 20 strains listed in Table 3.

Details regarding CNS strains:

MRCNS :
- *S. epidermidis* (1)
- *S. haemolyticus* (5)
- *S. simulans* (5)
- *S. warneri* (3)

MSCNS :
- *S. cohni cohnii* (1)
- *S. epidermidis* (1)
- *S. gallinarum (1)*
- *S. haemolyticus* (1)
- *S. lentus* (1)
- *S. lugdunensis* (1)
- *S. saccharolyticus* (1)
- *S. saprophyticus* (2)
- *S. xylosus (1)*

Table 20. Analytical sensitivity of tests performed on the Smart Cycler® thermocycler using the set of primers targeting MREP types i, ii, iii, iv, v and vii (SEQ ID NOs.: 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO.: 84) developed in the present invention for the detection and identification of MRSA

Staphylococcus aureus strain designation: Original	CCRI[a] (MREP type)	Detection limit (number of genome copies)
13370	CCRI-8894 (i)	2
ATCC 43300	CCRI-175 (ii)	2
35290	CCRI-1262 (iii)	2
ATCC 33592	CCRI-178 (iv)	2
R991282	CCRI-2025 (v)	2
SE-41-1	CCRI-9771 (vii)	2

[a] CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 21. Specificity and ubiquity tests performed on the Smart Cycler® thermocycler using the set of primers targeting MREP types i, ii, iii, iv, vi and vii (SEQ ID NOs.: 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO.: 84) developed in the present invention for the detection and identification of MRSA

Strains	PCR results for MREJ	
	Positive (%)	Negative (%)
MRSA - 23 strains[a]	19 (82.6)	4 (17.4)
MSSA - 25 strains	13 (52)	12 (48)
MRCNS - 26 strains	0	26 (100)
MSCNS - 8 strains	0	8 (100)

[a] MRSA strains include the 20 strains listed in Table 3.

Details regarding CNS strains:

MRCNS :
- *S. capitis* (2)
- *S. caprae* (1)
- *S. cohnii* (1)
- *S. epidermidis* (9)
- *S. haemolyticus* (5)
- *S. hominis* (2)
- *S. saprophyticus* (1)
- *S. sciuri* (2)
- *S. simulans* (1)
- *S. warneri* (2)

MSCNS :
- *S. cohni cohnii* (1)
- *S. epidermidis* (1)
- *S. haemolyticus* (1)
- *S. lugdunensis* (1)
- *S. saccharolyticus* (1)
- *S. saprophyticus* (2)
- *S. xylosus* (1)

Annex I: Strategy for the selection of specific amplification primers for types i and ii MREP

SEQ ID NO.:	Types i and ii MREP 2324 … 2358		orfX 2583 … 2607
2	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
1	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
17[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
18[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
19[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
20[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
21[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
22[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
23[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
24[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
25[a]	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
26	TAT **GTCAAAAATC ATGAACCTCA TTACTTATGA** TA...	CCT	**TGTGCAGGCC GTTTGATCCG** CC
33[c]		CtT	**gGTGtAaaCC aTTgGAgCCa** CC
34[c]		CCT	**caTGCAatCC aTTTGATC**
Selected sequence for type i MREP and ii primer (SEQ ID No.: 66)	**GTCAAAAATC ATGAACCTCA TTACTTATG**		
Selected sequence for *orfX* primer [b] (SEQ ID NO.: 64)			**TGTGCAGGCC GTTTGATCC**

The sequence positions refer to *SEQ ID NO.*: 2.

Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the displayed sequences.

[a] These sequences are the reverse-complements of SEQ ID NOs.: 17-25.
[b] This sequence is the reverse-complement of the selected primer.
[c] SEQ ID NOs.: 33 and 34 were obtained from CNS species.

Annex II: Strategy for the selection of a specific molecular beacon probe for the real-time detection of MREJ

	orfX 327 371
SEQ ID NO. :	
165	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
180	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
181	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
182	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
183	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
184	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
186	ACAAG **GACGT CTTACAACGC AGTAACTAtG** CACTA
174	ACAAG **GACGT CTTACAACGt AGTAACTACG** CACTA
175	ACAAG **GACGT CTTACAACGt AGTAACTACG** CACTA
178	ACAAG **GACGT CTTACAACGt AGTAACTACG** CACTA
176	ACAAG **GACGT CTTACAACGt AGTAACTACG** CACTA
173	ACAAG **GACGT CTTACAACGt AGTAACTACG** CACTA
177	ACAAG **GACGT CTTACAACGt AGTAACTACG** CACTA
169	ACAAG **GACGT CTTACAACGC AGTAACTACG** CACTA
199	ACAAG **GACGT CTTACAACGC AGTAACTACG** CACTA
33[a,b]	ACcAa **GACGT CTTACAACGC AGcAACTAtG** CttTA
34[a,b]	AtgAG **GACGT CTTACAACGC AGcAACTACG** CACTt
Selected sequence for *orfX* molecular beacon probes	
(SEQ ID NO.:163)[c]	**GACGT CTTACAACGC AGTAACTAtG**
(SEQ ID NO.:164)[c]	**GACGT CTTACAACGt AGTAACTACG**
(SEQ ID NO.: 84)[c]	**GACGT CTTACAACGC AGTAACTACG**

Nucleotide discrepancies between the *orfX* sequences and SEQ ID NO.: 84 are shown in lower-case. Other entries in the sequence listing also present similar variations. The stem of the molecular beacon probes are not shown for sake of clarity. The sequence positions refer to SEQ ID NO.:165.

[a] These sequences are the reverse-complements of SEQ ID NOs.: 33 and 34.
[b] SEQ ID NOs.: 33 and 34 were obtained from CNS species.
[c] The sequences presented are the reverse-complement of the selected molecular beacon probes.

CLAIMS

What is claimed is :

1. A method to detect the presence of a methicillin-resistant *Staphylococcus aureus* (MRSA) strain in a sample, said MRSA strain being resistant because of the presence of an SCC*mec* insert containing a *mecA* gene, said SCC*mec* being inserted in bacterial nucleic acids thereby generating a polymorphic right extremity junction (MREJ), said method comprising the step of annealing the nucleic acids of the sample with a plurality of probes and/or primers, characterized by:

(i) said primers and/or probes are specific for MRSA strains and capable of annealing with polymorphic MREJ nucleic acids, said polymorphic MREJ comprising MREJ types i to x; and

(ii) said primers and/or probes altogether can anneal with at least four MREJ types selected from MREJ types i to x.

2. The method of claim 1, wherein the primers and/or probes are all chosen to anneal under common annealing conditions.

3. The method of claim 2, wherein the primer and/or probes are placed altogether in the same physical enclosure.

4. The method of any one of claims 1 to 3, wherein the primers and/or probes have at least 10 nucleotides in length and are capable of annealing with MREJ types i to iii, defined in any one of SEQ ID NOs: 1, 20, 21, 22, 23, 24, 25, 41; 199 ; 2, 17, 18, 19, 26, 40, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 185, 186, 197 ; 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 104, 184, 198 ;
and with one or more of MREJ types iv to ix, having SEQ ID NOs: 42, 43, 44, 45, 46, 51 ; 47, 48, 49, 50 ; 171 ; 165, 166 ; 167 ; 168.

5. The method of any one of claims 1 to 4, wherein the primers and/or probes altogether can anneal with said SEQ ID NOs of MREJ types i to ix.

6. The method of any one of claims 1 to 5, wherein said primers and/or probes have the following sequences SEQ ID NOs:

66, 100, 101, 105, 52, 53, 54, 55, for the detection of MREJ type i
56, 57, 64, 71, 72, 73, 74, 75, 76,
70, 103, 130, 132, 158, 159, 59,
62, 126, 127, 128, 129, 131, 200,
201, 60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

66, 97, 99, 100, 101, 106, 117, for the detection of MREJ type ii
118, 124, 125, 52, 53, 54, 55, 56, 57
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

67, 98, 102, 107, 108 for the detection of MREJ type iii
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
58,
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

79, 77, 145, 147 for the detection of MREJ type iv
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
68
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

65, 80, 146, 154, 155 for the detection of MREJ type v
64, 71, 72, 73, 74, 75, 76,
70, 103, 130, 132, 158, 159
59, 62
126, 127

128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

202, 203, 204 for the detection of MREJ type vi
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

112, 113, 114, 119, 120, 121, 122 for the detection of MREJ type vii
, 123, 150, 151, 153
64, 71, 72, 73, 74, 75, 76, 70, 103,
130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

115, 116, 187, 188, 207, 208 for the detection of MREJ type viii
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

109, 148, 149, 205, 206 for the detection of MREJ type ix.
64, 71, 72, 73, 74, 75, 76
70, 103, 130, 132, 158, 159
59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

7. The method of claim 6, wherein primer pairs have the nucleotide sequence which are defined in SEQ ID NOs :

64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57	for the detection of type i MREJ
64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57	for the detection of type ii MREJ
64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58	for the detection of type iii MREJ
64/79	for the detection of type iv MREJ
64/80	for the detection of type v MREJ
64/204	for the detection of type vi MREJ
64/112, 64/113	for the detection of type vii MREJ
64/115, 64/116	for the detection of type viii MREJ
64/109	for the detection of type ix MREJ

8. The method of claim 7, further comprising probes having the following sequences: SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164 for the detection of MREJ types i to ix.

9. The method of any one of claims 6 to 8, wherein said primers and probes have the following nucleotide sequences:

vii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type i

viii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type ii

ix) SEQ ID NOs: 64, 67, 84, 163, 164 for the detection of MREJ type iii

x) SEQ ID NOs: 64, 79, 84, 163, 164 for the detection of MREJ type iv

xi) SEQ ID NOs: 64, 80, 84, 163, 164 for the detection of MREJ type v

xii) SEQ ID NOs: 64, 112, 84, 163, 164 for the detection of MREJ type vii.

10. The method of any one of claims 1 to 8, wherein said probes and primers are used together.

11. The method of claim 9 or 10, wherein said probes and/or primers are used together in the same physical enclosure.

12. A method for typing a MREJ of a MRSA strain, which comprises the steps of:

reproducing the method of any one of claims 1 to 11 with primers and/or probes specific for a determined MREJ type, and detecting an annealed probe and/or primer as an indication of the presence of a determined MREJ type.

13. A nucleic acid selected from:

vii) SEQ ID NOs: 42, 43, 44, 45, 46, 51 for sequence of MREJ type iv ;

viii) SEQ ID NOs: 47, 48, 49, 50 for sequence of MREJ type v ;

ix) SEQ ID NOs: 171 for sequence of MREJ type vi ;

x) SEQ ID NOs: 165, 166 for sequence of MREJ type vii ;

xi) SEQ ID NOs: 167 for sequence of MREJ type viii ;

xii) SEQ ID NOs: 168 for sequence of MREJ type ix.

14. An oligonucleotide of at least 10 nucleotides in length which hybridizes with the nucleic acid of claim 13 and which hybridizes with one or more MREJ of types selected from iv to ix.

15. An oligonucleotide pair which has the nucleotide sequences defined in any one of SEQ ID NOs:

64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57	for the detection of type i MREJ
64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57	for the detection of type ii MREJ

64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58	for the detection of type iii MREJ
64/79	for the detection of type iv MREJ
64/80	for the detection of type v MREJ
64/204	for the detection of type vi MREJ
64/112, 64/113	for the detection of type vii MREJ
64/115, 64/116	for the detection of type viii MREJ
64/109	for the detection of type ix MREJ

16. An oligonucleotide which has the nucleotide sequence defined in any one of SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164.

17. A composition of matter comprising primers and/or probes, the nucleotide sequences of which have at least 10 nucleotides in length which hybridize with any nucleic acid defined in claim 13, and which hybridize with one or more MREJ of types selected from iv to ix.

18. The composition of claim 17, which further comprises primers and/or probes, which hybridize with one or more MREJ of types selected from i to iii.

19. The composition of claim 18 or 19, wherein the primers pairs have the nucleotide sequences defined in SEQ ID NOs:

64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57	for the detection of type i MREJ
64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57	for the detection of type ii MREJ

64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58	for the detection of type iii MREJ
64/79	for the detection of type iv MREJ
64/80	for the detection of type v MREJ
64/204	for the detection of type vi MREJ
64/112, 64/113	for the detection of type vii MREJ
64/115, 64/116	for the detection of type viii MREJ
64/109	for the detection of type ix MREJ

20. The composition of claim 18, which further comprises probes, which SEQ ID NOs are: 32, 83, 84, 160, 161, 162, 163, 164.

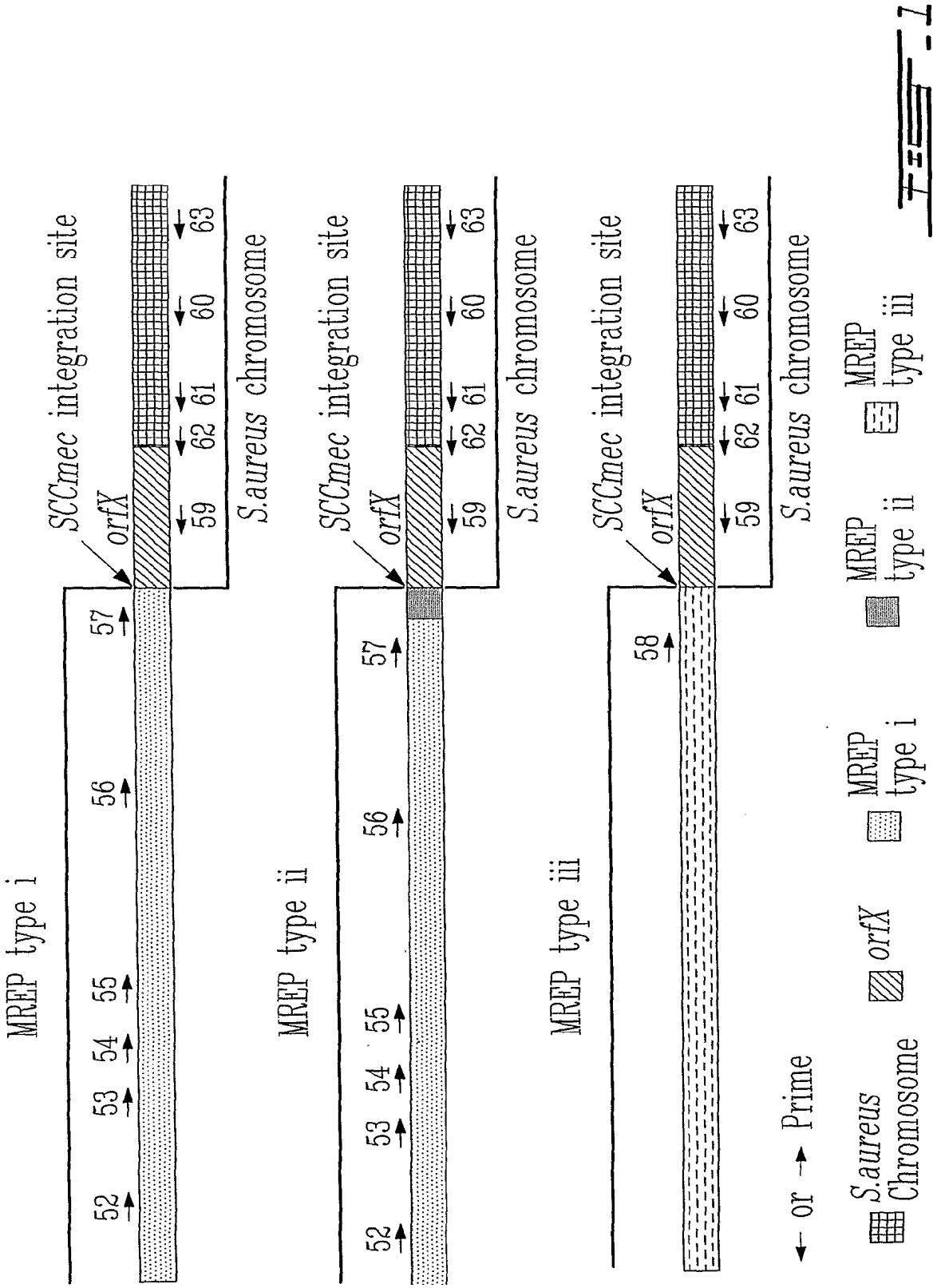
MREP type i
SCCmec integration site
orfX
S.aureus chromosome
52
53
54
55
56
57
59
62
61
60
63
MREP type ii
SCCmec integration site
orfX
S.aureus chromosome
52
53
54
55
56
57
59
62
61
60
63
MREP type iii
SCCmec integration site
orfX
S.aureus chromosome
58
59
62
61
60
63
MREP type i
MREP type ii
MREP type iii
orfX
S.aureus Chromosome
→ or ← Prime

FIG - 1

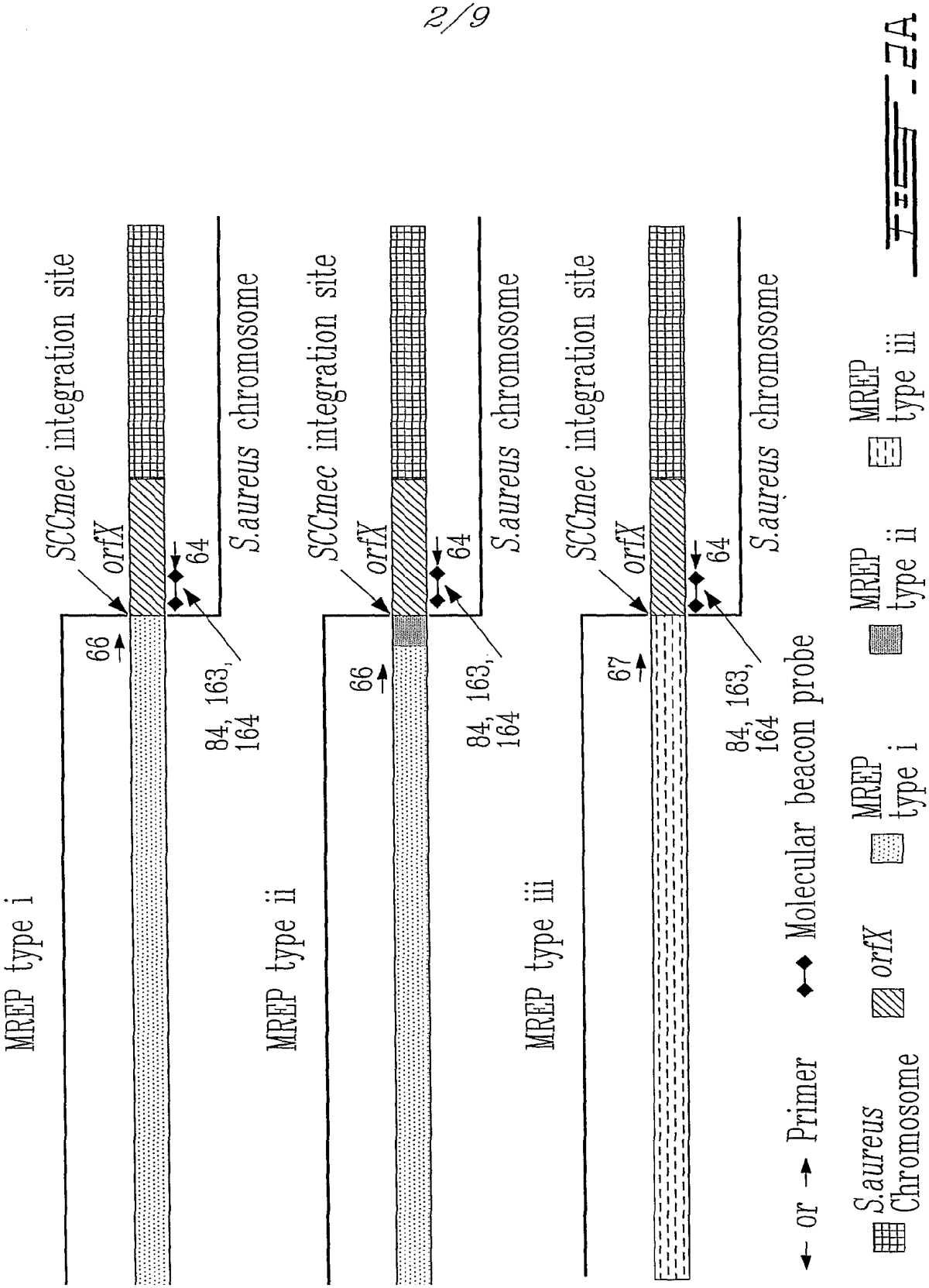
MREP type i
SCCmec integration site
orfX
66
64
84, 163, 164
S.aureus chromosome
MREP type ii
SCCmec integration site
orfX
66
64
84, 163, 164
S.aureus chromosome
MREP type iii
SCCmec integration site
orfX
67
64
84, 163, 164
S.aureus chromosome
→ or ← Primer
Molecular beacon probe
S.aureus Chromosome
orfX
MREP type i
MREP type ii
MREP type iii

Fig - 2A

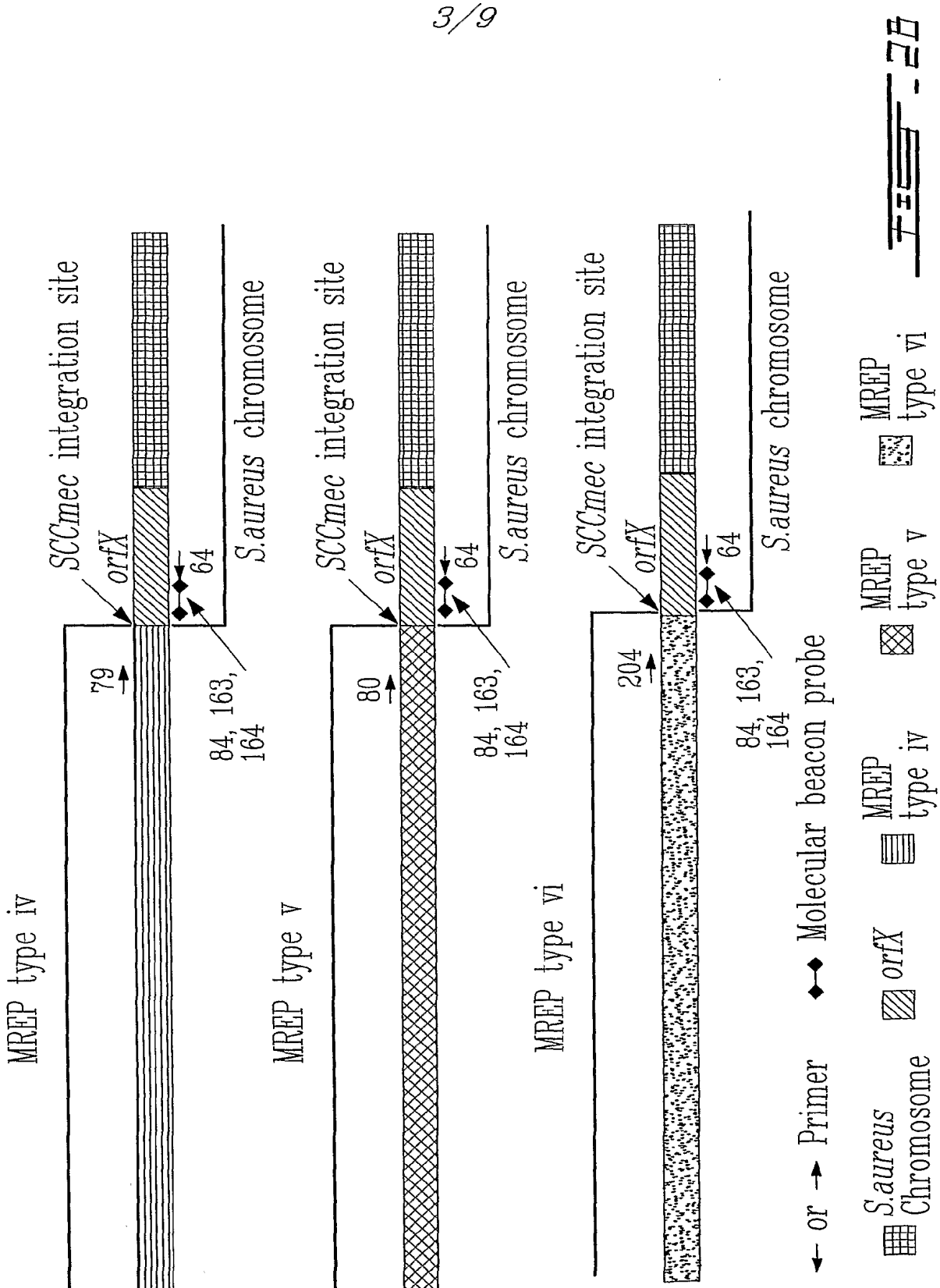
MREP type iv
SCCmec integration site
orfX
79
64
84, 163, 164
S.aureus chromosome
MREP type v
SCCmec integration site
orfX
80
64
84, 163, 164
S.aureus chromosome
MREP type vi
SCCmec integration site
orfX
204
64
84, 163, 164
S.aureus chromosome
← or → Primer
Molecular beacon probe
S.aureus Chromosome
orfX
MREP type iv
MREP type v
MREP type vi

Fig - 2B

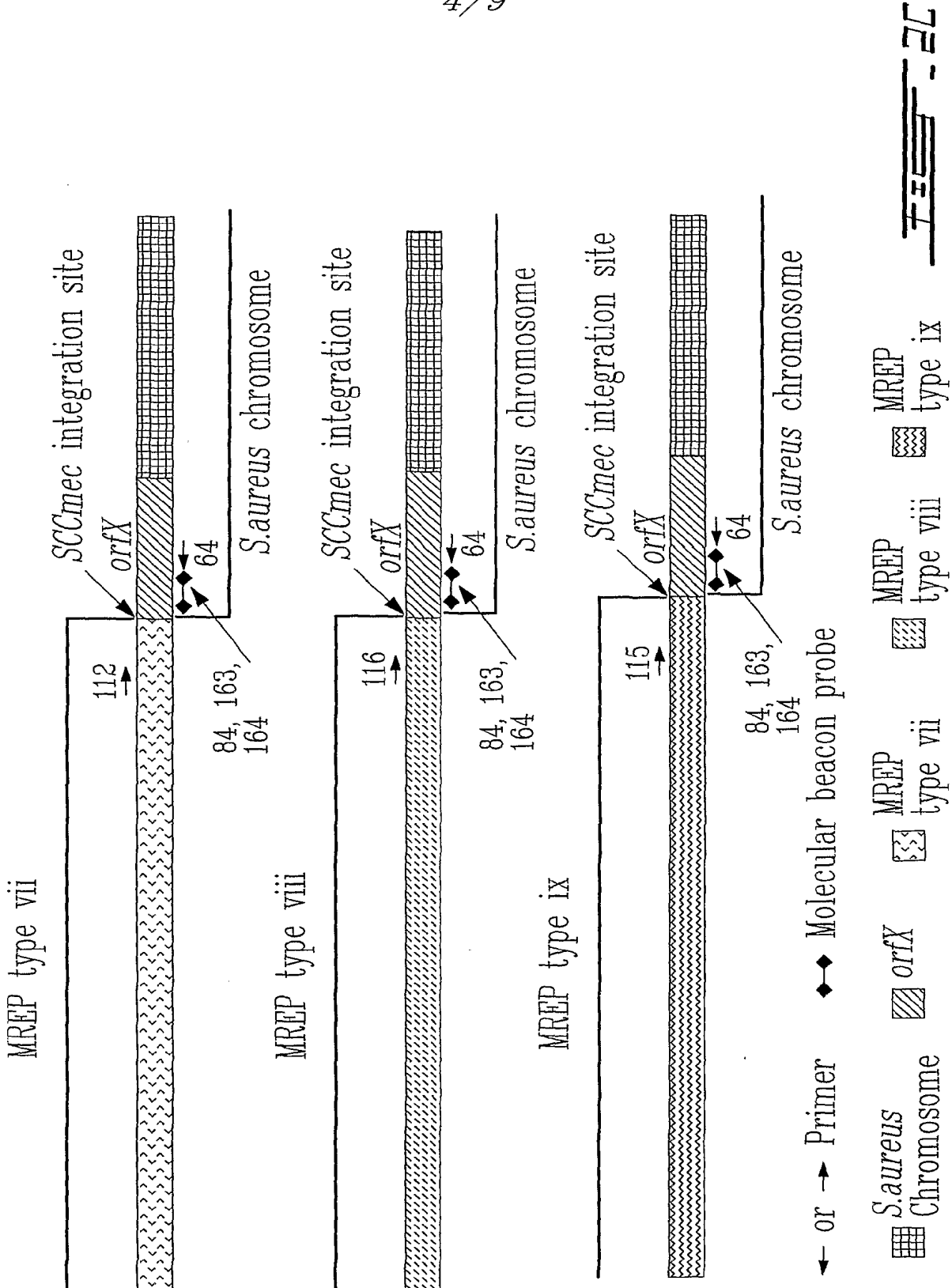
MREP type vii
SCCmec integration site
orfX
112
64
84, 163, 164
S.aureus chromosome
MREP type viii
SCCmec integration site
orfX
116
64
84, 163, 164
S.aureus chromosome
MREP type ix
SCCmec integration site
orfX
115
64
84, 163, 164
S.aureus chromosome
← or → Primer
Molecular beacon probe
S.aureus Chromosome
orfX
MREP type vii
MREP type viii
MREP type ix

Fig. 3E

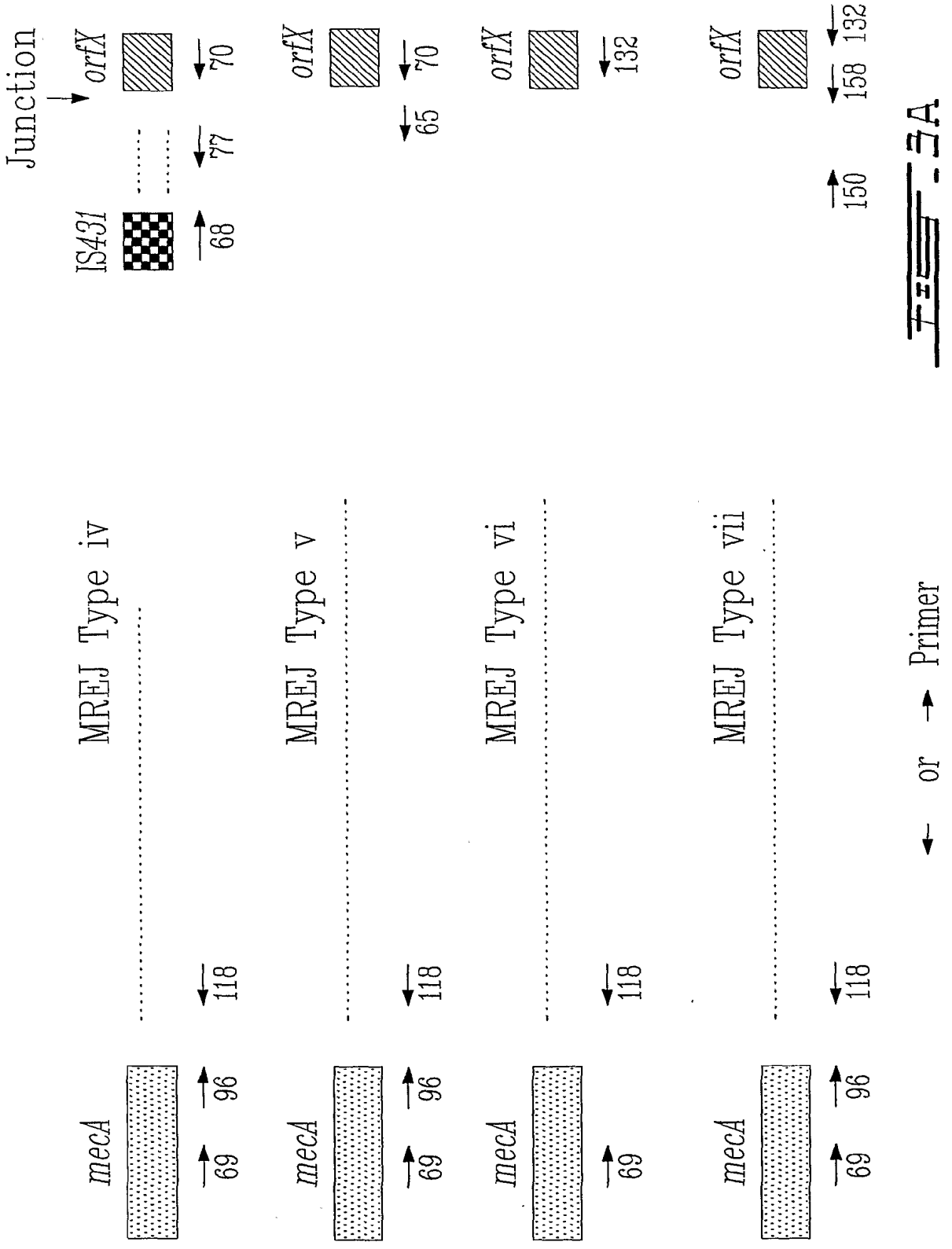
Junction
orfX
IS431
70
77
68
65
132
158
150
MREJ Type iv
MREJ Type v
MREJ Type vi
MREJ Type vii
mecA
118
96
69
or
Primer

FIG. 3A

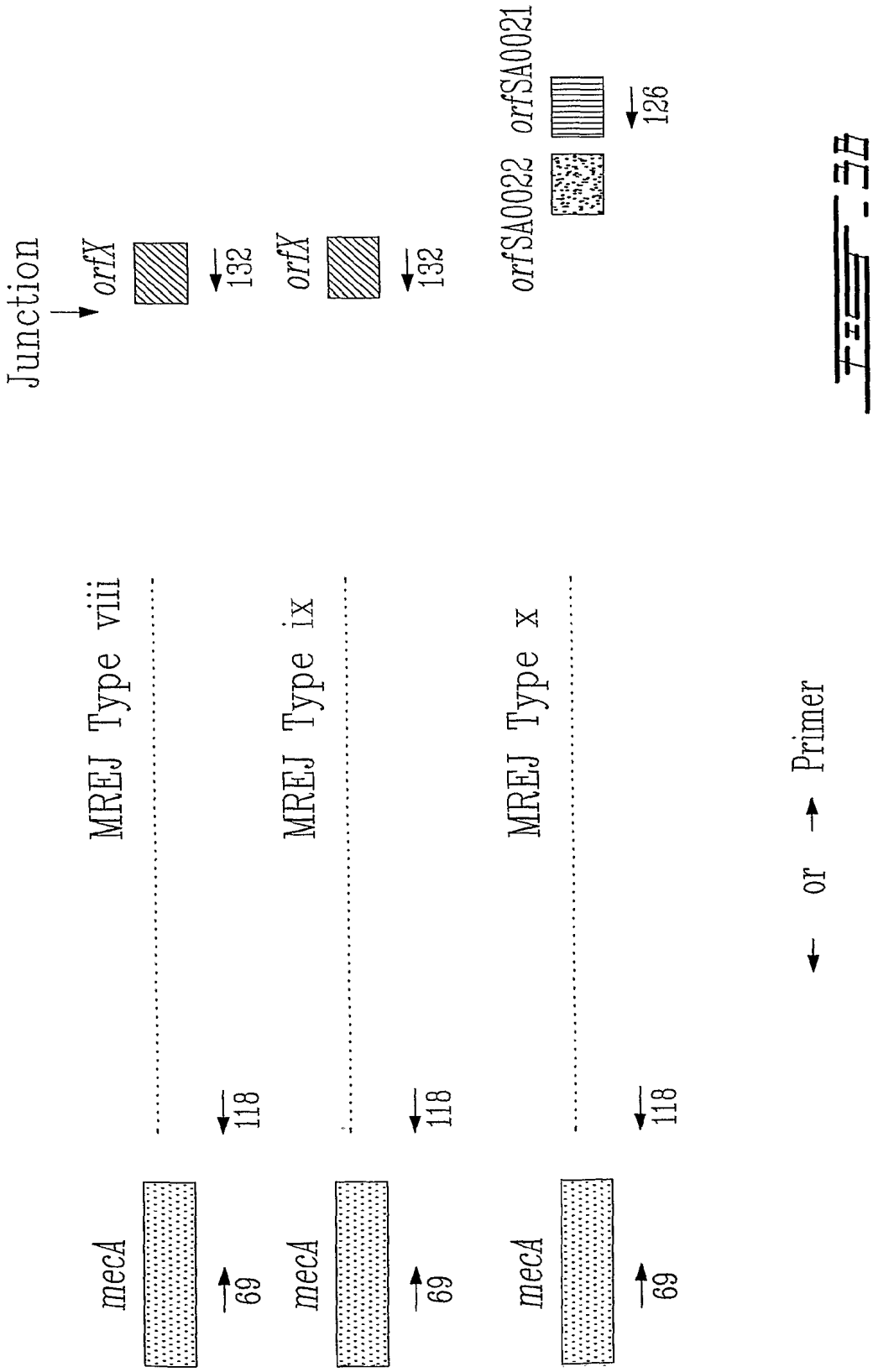
Junction
orfX
132
orfX
132
orfSA0022
orfSA0021
126
MREJ Type viii
MREJ Type ix
MREJ Type x
118
118
118
mecA
mecA
mecA
69
69
69
← or → Primer

FIG - 3B

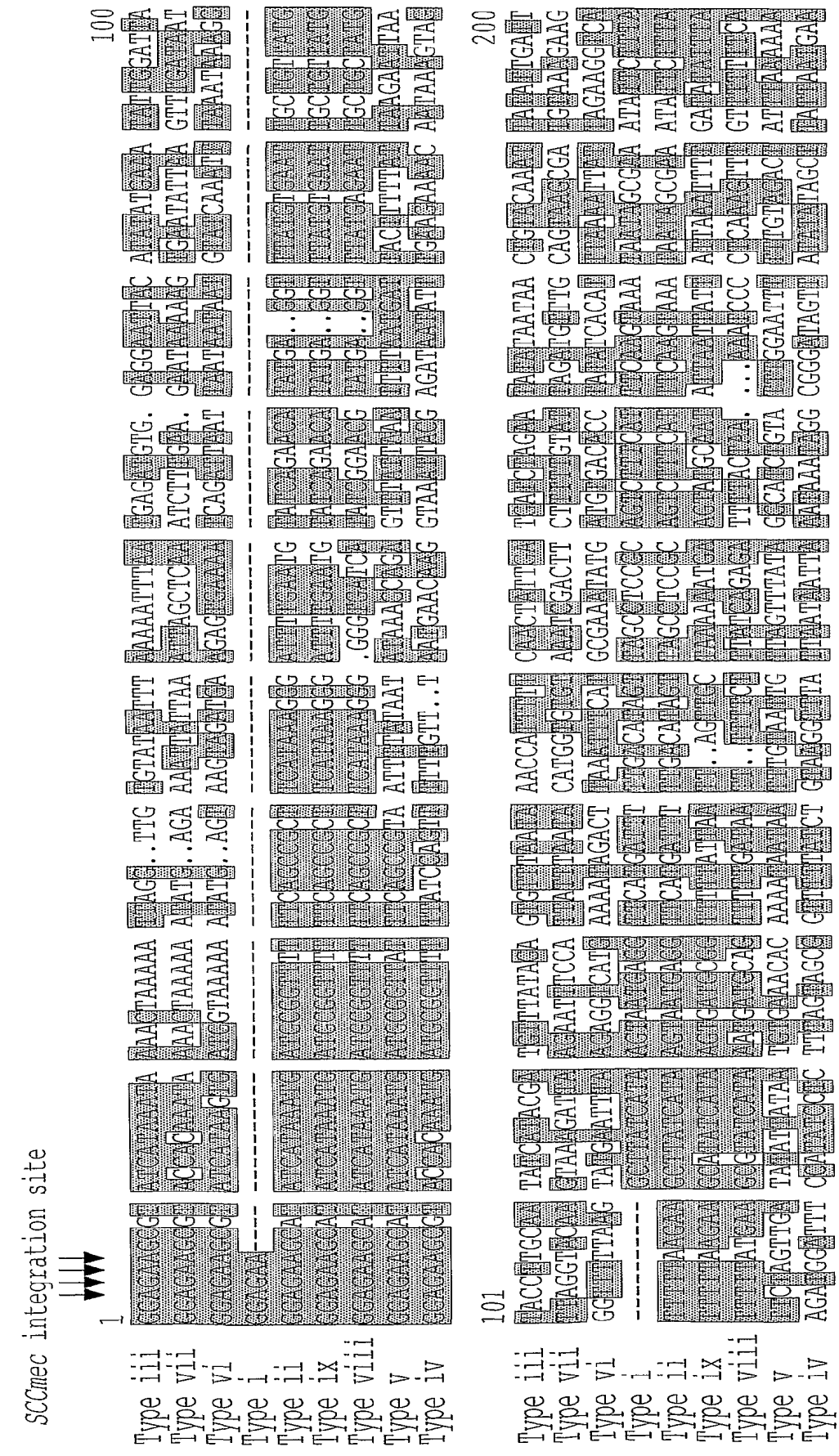
SCCmec integration site
Type iii
Type vii
Type vi
Type i
Type ii
Type ix
Type viii
Type v
Type iv
1
100
101
200

Fig - 4A

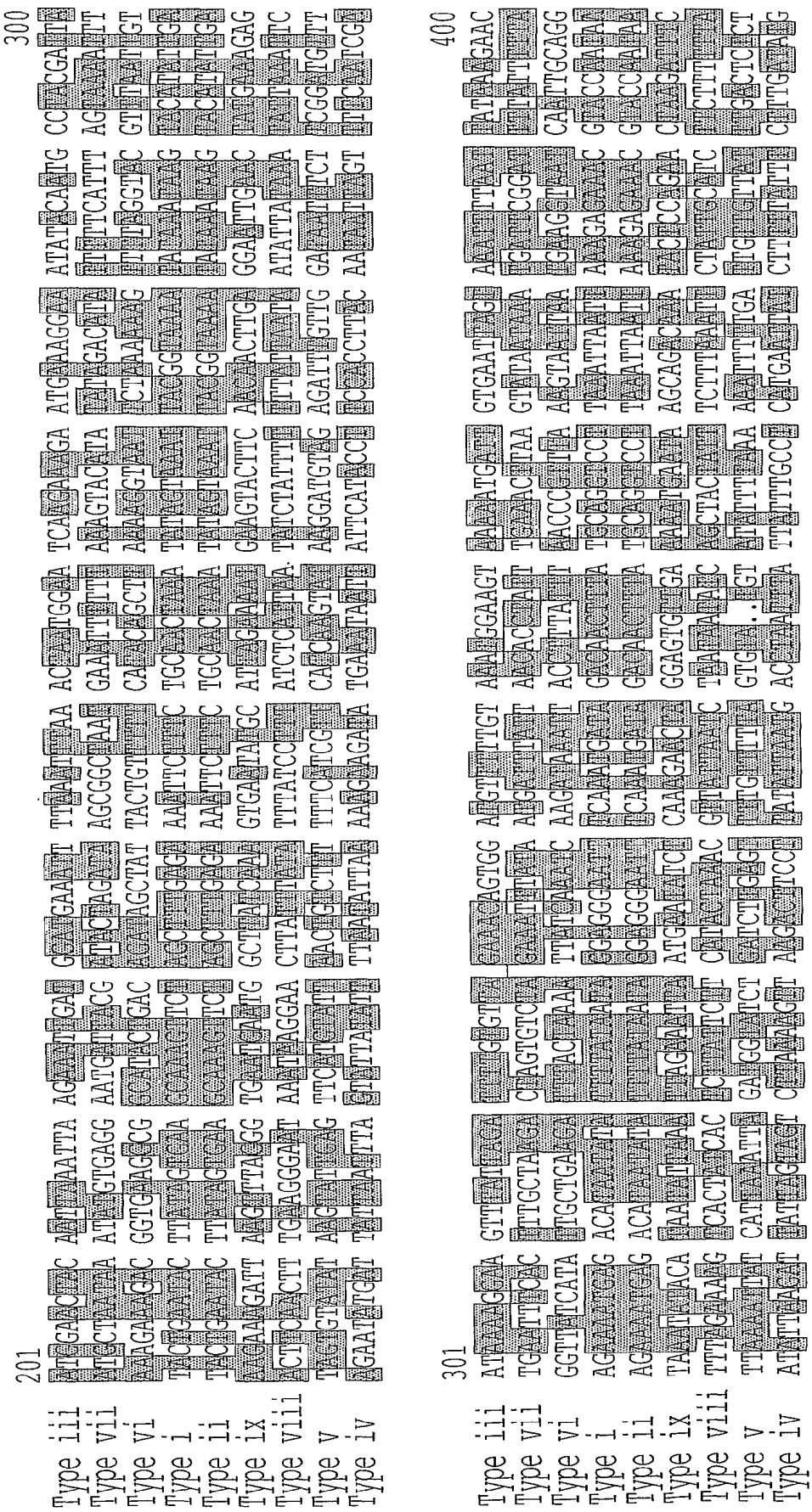

Fig - 4B

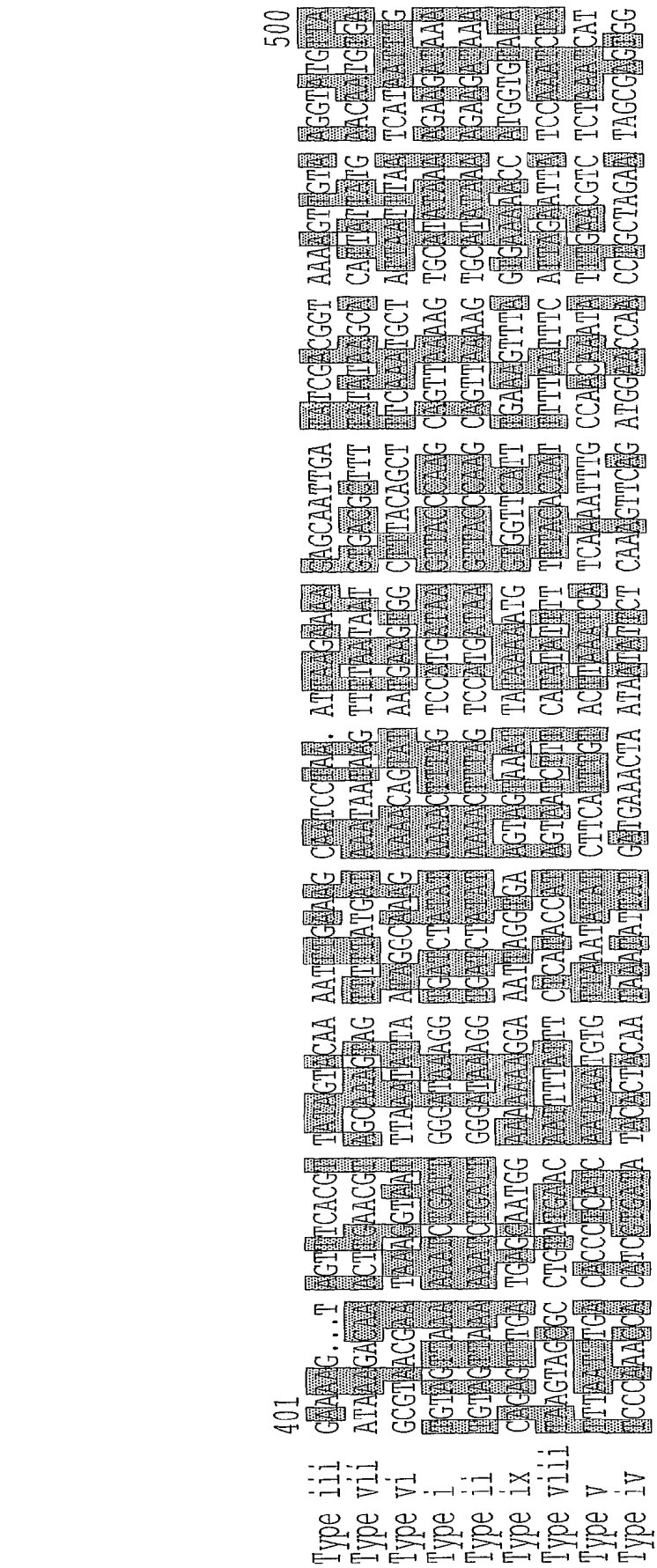

Fig - 4C

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

HULETSKY, Ann [1], 1231 Av des Pins, Sillery, Quebec, Canada, G1S 4J3
ROSSBACH, Valery [1], 55 Rue du Sauternes, Aylmer, Quebec, Canada, J9H 3W7

[1]:Canadian citizenship

(ii) TITLE OF THE INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS

(iii) NUMBER OF SEQUENCES: 233

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(v) COMPUTER READABLE:

(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING:
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:
(B) REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE:
(B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3050 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC 10442
(C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

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GTACATCGAA ATATCTGAAT AACCTCATTG AGCAAGATCA CCGTCATATT     250
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TACACATTAT CTTATCTGCT CTTTATCACC ATAAAAATAG AAAAAACAAG     950
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AGCGCTAATT TTTCTCCAAC TTTACCGGTT AATTTATTCT CTTTATTTGA    1550
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AGTATATGCC TTCTCCTTCC GGATGAAAAA GATATACCAA ATAATATCCA     2100
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TTTACTATAG TTCCCAGTAG CAACCTTCCC TACAACTGAA TATTTATCTT     2200
CTTTTATATG CACTTTTAAC TGCTTGGGTA ACTTATCATG GACTAAAGTT     2250
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ACGTTTCTCT TTAATTAATT TAAGGACCTG CATAAAGTTG TCTATCATTT     2350
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TACTTATTTA TATTTTACCG TAATTTACTA TATTTAGTTG CAGAAAGAAT     2450
TTTCTCAAAG CTAGAACTTT GCTTCACTAT AAGTATTCAG TATAAAGAAT     2500
ATTTCGCTAT TATTTACTTG AAATGAAAGA CTGCGGAGGC TAACTATGTC     2550
AAAAATCATG AACCTCATTA CTTATGATAA GCTTCTCCTC GCATAATCTT     2600
AAATGCTCTG TACACTTGTT CAATTAACAC AACCCGCATC ATTTGATGTG     2650
GGAATGTCAT TTTGCTGAAT GATAGTGCGT AGTTACTGCG TTGTAAGACG     2700
TCCTTGTGCA GGCCGTTTGA TCCGCCAATG ACGAAAACAA AGTCGCTTTG     2750
CCCTTGGGTC ATGCGTTGGT TCAATTCTTG GGCCAATCCT TCGGAAGATA     2800
GCATCTTTCC TTGTATTTCT AATGTAATGA CTGTGGATTG TGGTTTGATT     2850
TTGGCTAGTA TTCGTTGGCC TTCTTTTTCT TTTACTTGCT CAATTTCTTT     2900
GTCACTCATA TTTTCTGGTG CTTTTTCGTC TGGAACTTCT ATGATGTCTA     2950
TCTTGGTGTA TGGGCCTAAA CGTTTTTCAT ATTCTGCTAT GGCTTGCTTC     3000
CAATATTTCT CTTTTAGTTT CCCTACAGCT AAAATGGTGA TTTTCATGTC     3050
```

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3050 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: N315
- (C) ACCESSION NUMBER:Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

```
ACCTCATTGA GCAAGATCAC CGTCATATTA AAGTAAGAAA GACAAGGTAT      50
CAAAGTATCA ATACAGCAAA GAATACTTTA AAAGGTATTG AATGTATTTA     100
CGCTCTATAT AAAAAGAACC GCAGGTCTCT TCAGATCTAC GGATTTTCGC     150
CATGCCACGA AATTAGCATC ATGCTAGCAA GTTAAGCGAA CACTGACATG     200
ATAAATTAGT GGTTAGCTAT ATTTTTTTAC TTTGCAACAG AACCGAAAAT     250
AATCTCTTCA ATTTATTTTT ATATGAATCC TGTGACTCAA TGATTGTAAT     300
```

```
ATCTAAAGAT TTCAGTTCAT CATAGACAAT GTTCTTTTCA ACATTTTTTA      350
TAGCAAATTG ATTAAATAAA TTCTCTAATT TCTCCCGTTT GATTTCACTA      400
CCATAGATTA TATTATCATT GATATAGTCA ATGAATAATG ACAAATTATC      450
ACTCATAACA GTCCCAACCC CTTTCTTTTG ATAGACTAAT TATCTTCATC      500
ATTGTAAAAC AAATTACACC CTTTAAATTT AACTCAACTT AAATATCGAC      550
AAATTAAAAA ACAATAAAAT TACTTGAATA TTATTCATAA TATATTAACA      600
ACTTTATTAT ACTGCTCTTT ATATATAAAA TCATTAATAA TTAAACAAGC      650
CTTAAAATAT TTAACTTTTT TGTGATTATT ACACATTATC TTATCTGCTC      700
TTTATCACCA TAAAAATAGA AAAAACAAGA TTCCTAAAGA ATATAGGAAT      750
CTTGTTTCAG ACTGTGGACA AACTGATTTT TTATCAGTTA GCTTATTTAG      800
AAAGTTTTAT TTAAATTACA GTTTCTATTT TTATTAGATC ACAATTTTAT      850
TTTAGCTCTT GTTCAAGTAA TCATTTTTCG CCAAAAACTT TATACTGAAT      900
AGCTTCTACA TTAAATACTT TGTCAATGAG ATCATCTACA TCTTTAAATT      950
CAGAATAATT TGCATATGGA TCTATAAAAT AAAATTGTGG TTCTTTACCG     1000
GAAACATTAA ATATTCTTAA TATTAAATAT TTCTGCTTAT ATTCTTTCAT     1050
AGCAAACATT TCATTTAGCG ACATAAAAAA TGGTTCCTCA ATACTAGAAG     1100
ATGTAGATGT TTTAATTTCA ATAAATTTTT CTACAGCTTT ATCTGTATTT     1150
GTTGGATCAA AAGCTACTAA ATCATAGCCA TGACCGTGTT GAGAGCCTGG     1200
ATTATCATTT AAAATATTCC TAAACTGTTC TTTCTTATCT TCGTCTATTT     1250
TATTATCAAT TAGCTCATTA AAGTAATTTA GCGCTAATTT TTCTCCAACT     1300
TTACCGGTTA ATTTATTCTC TTTATTTGAT TTTTCAATTT CTGAATCATT     1350
TTTAGTAGTC TTTGATACAC CTTTTTTATA TTTTGGAATT ATTCCTTTAG     1400
GTGCTTCCAC TTCCTTGAGT GTCTTATCTT TTTGTGCTGT TCTAATTTCT     1450
TCAATTTCGC TGTCTTCCTG TATTTCGTCT ATGCTATTGA CCAAGCTATC     1500
ATAGGATGTT TTTGTAACTT TTGAAGCTAA TTCATTAAAT AGTTCTAAAA     1550
ATTTCTTTAA ATCCTCTAGC ATATCTTCTT CTGTGAATCC TTCATTCAAA     1600
TCATAATATT TGAATCTTAT TGATCCATGA GAATATCCTG ATGGATAATC     1650
ATTTTTTAAA TCATAAGATG AATCTTTATT TTCTGCGTAA TAAAATCTTC     1700
CAGTATTAAA TTCATTTGAT GTAATATATT TATTGAGTTC GGAAGATAAA     1750
GTTAATGCTC TTTGTTTTGC AGCATTTTTA TCCCGCGGAA ACATATCACT     1800
TATCTTTGAC CATCCTTGAT TCAAAGATAA GTATATGCCT TCTCCTTCCG     1850
GATGAAAAAG ATATACCAAA TAATATCCAT CCTTTGTTTC TTTTGTTATA     1900
TTCTCATCAT ATATTGAAAT CCAAGGAACT TTACTATAGT TCCCAGTAGC     1950
AACCTTCCCT ACAACTGAAT ATTTATCTTC TTTTATATGC ACTTTTAACT     2000
GCTTGGGTAA CTTATCATGG ACTAAAGTTT TATATAGATC ACCTTTATCC     2050
CAATCAGATT TTTTAACTAC ATTATTGGTA CGTTTCTCTT TAATTAATTT     2100
AAGGACCTGC ATAAAGTTGT CTATCATTTG AAATTCCCTC CTATTATAAA     2150
ATATATTATG TCTCATTTTC TTCAATATGT ACTTATTTAT ATTTTACCGT     2200
AATTTACTAT ATTTAGTTGC AGAAAGAATT TTCTCAAAGC TAGAACTTTG     2250
CTTCACTATA AGTATTCAGT ATAAAGAATA TTTCGCTATT ATTTACTTGA     2300
AATGAAAGAC TGCGGAGGCT AACTATGTCA AAAATCATGA ACCTCATTAC     2350
TTATGATAAG CTTCTTAAAA ACATAACAGC AATTCACATA AACCTCATAT     2400
GTTCTGATAC ATTCAAAATC CCTTTATGAA GCGGCTGAAA AAACCGCATC     2450
ATTTATGATA TGCTTCTCCA CGCATAATCT TAAATGCTCT ATACACTTGC     2500
TCAATTAACA CAACCCGCAT CATTTGATGT GGGAATGTCA TTTTGCTGAA     2550
TGATAGTGCG TAGTTACTGC GTTGTAAGAC GTCCTTGTGC AGGCCGTTTG     2600
ATCCGCCAAT GACGAATACA AAGTCGCTTT GCCCTTGGGT CATGCGTTGG     2650
TTCAATTCTT GGGCCAATCC TTCGGAAGAT AGCATCTTTC CTTGTATTTC     2700
TAATGTAATG ACTGTGGATT GTGGTTTAAT TTTGGCTAGT ATTCGTTGGC     2750
CTTCTTTTTC TTTTACTTGC TCAATTTCTT TGTCGCTCAT ATTTTCTGGT     2800
GCTTTTTCGT CTGGAACTTC TATGATGTCT ATCTTGGTGT ATGGGCCTAA     2850
ACGTTTTTCA TATTCTGCTA TGGCTTGCTT CCAATATTTC TCTTTTAGTT     2900
```

TCCCTACAGC TAAAATGGTG ATTTTCATGT CGTTTGGTCC TCCAAATTGT 2950
TATCAACTTT CCAGTTATCC ACAAGTTATT AACTTGTTCA CACTGTTCCC 3000
TCTTATTATA CCAATATTTT TTGCAGTTTT TGATATTTTC CTGACATTTA 3050

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3183 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC 8325
(C) ACCESSION NUMBER: AB014440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

CTGCAGAGGT AATTATTCCA AACAATACCA TTGATTTCAA AGGAGAAAGA 50
GATGACGTTA GAACGCGTGA AACAAATTTA GGAAACGCGA TTGCAGATGC 100
TATGGAAGCG TATGGCGTTA AGAATTTCTC TAAAAAGACT GACTTTGCCG 150
TGACAAATGG TGGAGGTATT CGTGCCTCTA TCGCAAAAGG TAAGGTGACA 200
CGCTATGATT TAATCTCAGT ATTACCATTT GGAAATACGA TTGCGCAAAT 250
TGATGTAAAA GGTTCAGACG TCTGGACGGC TTTCGAACAT AGTTTAGGCG 300
CACCAACAAC ACAAAAGGAC GGTAAGACAG TGTTAACAGC GAATGGCGGT 350
TTACTACATA TCTCTGATTC AATCCGTGTT TACTATGATA TAAATAAACC 400
GTCTGGCAAA CGAATTAATG CTATTCAAAT TTTAAATAAA GAGACAGGTA 450
AGTTTGAAAA TATTGATTTA AAACGTGTAT ATCACGTAAC GATGAATGAC 500
TTCACAGCAT CAGGTGGCGA CGGATATAGT ATGTTCGGTG GTCCTAGAGA 550
AGAAGGTATT TCATTAGATC AAGTACTAGC AAGTTATTTA AAAACAGCTA 600
ACTTAGCTAA GTATGATACG ACAGAACCAC AACGTATGTT ATTAGGTAAA 650
CCAGCAGTAA GTGAACAACC AGCTAAAGGA CAACAAGGTA GCAAAGGTAG 700
TAAGTCTGGT AAAGATACAC AACCAATTGG TGACGACAAA GTGATGGATC 750
CAGCGAAAAA ACCAGCTCCA GGTAAAGTTG TTTTGTTGCT AGCGCATAGA 800
GGAACTGTTA GTAGCGGTAC AGAAGGTTCT GGTCGCACAA TAGAAGGAGC 850
TACTGTATCA AGCAAGAGTG GGAAACAATT GGCTAGAATG TCAGTGCCTA 900
AAGGTAGCGC GCATGAGAAA CAGTTACCAA AAACTGGAAC TAATCAAAGT 950
TCAAGCCCAG AAGCGATGTT TGTATTATTA GCAGGTATAG GTTTAATCGC 1000
GACTGTACGA CGTAGAAAAG CTAGCTAAAA TATATTGAAA ATAATACTAC 1050
TGTATTTCTT AAATAAGAGG TACGGTAGTG TTTTTTTATG AAAAAAAGCG 1100
ATAACCGTTG ATAAATATGG GATATAAAAA CGAGGATAAG TAATAAGACA 1150
TCAAGGTGTT TATCCACAGA AATGGGGATA GTTATCCAGA ATTGTGTACA 1200
ATTTAAAGAG AAATACCCAC AATGCCCACA GAGTTATCCA CAAATACACA 1250
GGTTATACAC TAAAAATCGG GCATAAATGT CAGGAAAATA TCAAAAACTG 1300
CAAAAAATAT TGGTATAATA AGAGGGAACA GTGTGAACAA GTTAATAACT 1350
TGTGGATAAC TGGAAAGTTG ATAACAATTT GGAGGACCAA ACGACATGAA 1400
AATCACCATT TTAGCTGTAG GGAAACTAAA AGAGAAATAT TGGAAGCAAG 1450

```
CCATAGCAGA ATATGAAAAA CGTTTAGGCC CATACACCAA GATAGACATC      1500
ATAGAAGTTC CAGACGAAAA AGCACCAGAA AATATGAGTG ACAAAGAAAT      1550
TGAGCAAGTA AAAGAAAAAG AAGGCCAACG AATACTAGCC AAAATCAAAC      1600
CACAATCCAC AGTCATTACA TTAGAAATAC AAGGAAAGAT GCTATCTTCC      1650
GAAGGATTGG CCCAAGAATT GAACCAACGC ATGACCCAAG GGCAAAGCGA      1700
CTTTGTTTTC GTCATTGGCG GATCAAACGG CCTGCACAAG GACGTCTTAC      1750
AACGCAGTAA CTACGCACTA TCATTCAGCA AAATGACATT CCCACATCAA      1800
ATGATGCGGG TTGTGTTAAT TGAACAAGTG TACAGAGCAT TTAAGATTAT      1850
GCGAGGAGAG GCGTATCATA AGTAAAACTA AAAAATTCTG TATGAGGAGA      1900
TAATAATTTG GAGGGTGTTA AATGGTGGAC ATTAAATCCA CGTTCATTCA      1950
ATATATAAGA TATATCACGA TAATTGCGCA TATAACTTAA GTAGTAGCTA      2000
ACAGTTGAAA TTAGGCCCTA TCAAATTGGT TTATATCTAA AATGATTAAT      2050
ATAGAATGCT TCTTTTTGTC CTTATTAAAT TATAAAAGTA ACTTTGCAAT      2100
AGAAACAGTT ATTTCATAAT CAACAGTCAT TGACGTAGCT AAGTAATGAT      2150
AAATAATCAT AAATAAAATT ACAGATATTG ACAAAAAATA GTAAATATTC      2200
CAATGAAGTT TCAAAAGAAC AATTCCAAGA AATTGAGAAT GTAAATAATA      2250
AGGTCAAAGA ATTTTATTAA GATTTGAAAG AGTATCAATC AAGAAAGATG      2300
TAGTTTTTTA ATAAACTATT TGGAAAATAA TTATCATAAT TTAAAAACTG      2350
ACAATTTGCG AGACTCATAA AATGTAATAA TGGAAATAGA TGTAAAATAT      2400
AATTAAGGGG TGTAATATGA AGATTAATAT TTATAAATCT ATTTATAATT      2450
TTCAGGAAAC AAATACAAAT TTTTTAGAGA ATCTAGAATC TTTAAATGAT      2500
GACAATTATG AACTGCTTAA TGATAAAGAA CTTGTTAGTG ATTCAAATGA      2550
ATTAAAATTA ATTAGTAAAG TTTATATACG TAAAAAAGAC AAAAAACTAT      2600
TAGATTGGCA ATTATTAATA AAGAATGTAT ACCTAGATAC TGAAGAAGAT      2650
GACAATTTAT TTTCAGAATC CGGTCATCAT TTTGATGCAA TATTATTTCT      2700
CAAAGAAGAT ACTACATTAC AAAATAATGT ATATATTATA CCTTTTGGAC      2750
AAGCATATCA TGATATAAAT AATTTGATTG ATTATGACTT CGGAATTGAT      2800
TTTGCAGAAA GAGCAATCAA AAATGAAGAC ATAGTTAATA AAAATGTTAA      2850
TTTTTTTCAA CAAAACAGGC TTAAAGAGAT TGTTAATTAT AGAAGGAATA      2900
GTGTAGATTA CGTTAGACCT TCAGAATCTT ATATATCAGT CCAAGGACAT      2950
CCACAGAATC CTCAAATTTT TGGAAAAACA ATGACTTGTG GTACAAGTAT      3000
TTCATTGCGT GTACCGAATA GAAAGCAGCA ATTCATAGAT AAAATTAGTG      3050
TGATAATCAA AGAAATAAAC GCTATTATTA ATCTTCCTCA AAAAATTAGT      3100
GAATTTCCTA GAATAGTAAC TTTAAAAGAC TTGAATAAAA TAGAAGTATT      3150
AGATACTTTA TTGCTAAAAA AACTATCGAA TTC                        3183
```

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 86/560
- (C) ACCESSION NUMBER: AB013471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACA                              479
```

2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 86/961
(C) ACCESSION NUMBER: AB013472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATAAC ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACAG                             480
```

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/3907
(C) ACCESSION NUMBER: AB013473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATCCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTGTGT TAGAAACAGT                             480
```

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 86/2652
(C) ACCESSION NUMBER: AB013474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACAG                             480
```

2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/1340
(C) ACCESSION NUMBER: AB013475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

```
GGCGGATCAA ACGGCCTGCA CAAGGACGTC TTACAACGCA GTAACTACGC        50
ACTATCATTC AGCAAAATGA CATTCCCACA TCAAATGATG CGGGTTGTGT       100
TAATTGAACA AGTGTACAGA GCATTTAAGA TTATGCGTGG AGAAGCGTAT       150
CATAAATAAA ACTAAAAATT AGGTTGTGTA TAATTTAAAA ATCTAATGAG       200
ATGTGGAGGA ATTACATATA TGAAATATTG GATTATNCCT TGCAATATCA       250
TACGATGTTT ATAGAGTGTT TAATAAACCA TTTTTCAACT ATTGATGATC       300
TACAATATA                                                   309
```

2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/1762
(C) ACCESSION NUMBER: AB013476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

```
TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG CAGTAACTAC        50
GCACTATCAT TCAGCAAAAT GACATTCCCA CATCAAATGA TGCGGGTTGT       100
GTTAATTGAA CAAGTGTACA GAGCATTTAA GATTATGCGT GGAGAAGCGT       150
ATCATAAATA AAACTAAAAA TTAGGTTGTG TATAATTTAA AAATTTAATG       200
AGATGTGGAG GAATTACATA TATGAAATAT TGGATTATAC CTTGCAATAT       250
CATACGATGT TTATAGAGTG TTTAATAAAC CATTTTTCAA CTATTGATGA       300
```

```
TCTAGAATAT ATAATAACTG TACAAATTAT ATTGATTATG GAACTACAAT      350
TAAATTAAGA AATTGATGAT GAAATTTTAA ATTTAAACTA ATGGAATCAA      400
GAAAGAATGA AAGGAAATAT ACAATGCCTA CGATTAATAA AAGGAAGTTT      450
ATTAGATTTT GTGTTAGAAA C                                    471
```

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH:480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: AB013477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG       50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC      100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA      150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA      200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT      250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA      300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA      350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG      400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG      450
GAAGTTTATT AGATTTTGTG TTAGAAACAG                           480
```

2) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2111
- (C) ACCESSION NUMBER: AB013478

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 11

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACAG                            480
```

2)INFORMATION FOR SEQ ID NO: 12

(i) (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/5495
(C) ACCESSION NUMBER: AB013479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACAG                            480
```

2)INFORMATION FOR SEQ ID NO: 13

(i) (A) LENGTH: 478 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/1836
(C) ACCESSION NUMBER: AB013480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAAC                               478
```

2) INFORMATION FOR SEQ ID NO: 14·

(i) (A) LENGTH: 479 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/2147
(C) ACCESSION NUMBER: AB013481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACA                              479
```

2) INFORMATION FOR SEQ ID NO: 15

(i) (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/3619
(C) ACCESSION NUMBER: AB013482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCNCGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
GAAGTTTATT AGATTTTGTG TTAGAAACAG                             480
```

2) INFORMATION FOR SEQ ID NO: 16

(i) (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/3566
(C) ACCESSION NUMBER: AB013483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCGTATC ATAAATAAAA CTAAAAATTA GGTTGTGTAT AATTTAAAAA       200
TTTAATGAGA TGTGGAGGAA TTACATATAT GAAATATTGG ATTATACCTT       250
GCAATATCAT ACGATGTTTA TAGAGTGTTT AATAAACCAT TTTTCAACTA       300
TTGATGATCT AGAATATATA ATAACTGTAC AAATTATATT GATTATGGAA       350
CTACAATTAA ATTAAGAAAT TGATGATGAA ATTTTAAATT TAAACTAATG       400
GAATCAAGAA AGAATGAAAG GAAATATACA ATGCCTACGA TTAATAAAAG       450
```

GAAGTTTATT AGATTTTGTG TTAGAAACAG 480

2) INFORMATION FOR SEQ ID NO: 17

(i) (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/2232
(C) ACCESSION NUMBER: AB014402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG 50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC 100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA 150
GAAGCATATC ATAAATGATG CGGTTTTTTC AGCCGCTTCA TAAAGGGATT 200
TTGAATGTAT CAGAACATAT GAGGTTTATG TGAATTGCTG TTATGTTTTT 250
AAGAAGCTTA TCATAAGTAA TGAGGTTCAT GATTTTTGAC ATAGTTAGCC 300
TCCGCAGTCT TTCATTTCAA GTAAATAATA GCGAAATATT CTTTATACTG 350
AATACTTATA GTGAAGCAAA GTTCTAGCTT TGAGAAAATT CTTTCTGCAA 400
CTAAATATAG TAAATTACGG TAAAATATAA ATAAGTACAT ATTGAAGAAA 450
ATGAGACATA ATATATTTTA TAATAGGAGG 480

2) INFORMATION FOR SEQ ID NO: 18

(i) (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/2235
(C) ACCESSION NUMBER: AB014403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG 50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC 100
GGGTTGTGTT AATTGAGCAA GTGTATAGAG CATTTAAGAT TATGCGTGGA 150

```
GAAGCATATC ATAAATGATG CGGTTTTTTC AGCCGCTTCA TAAAGGGATT      200
TTGAATGTAT CAGAACATAT GAGGTTTATG TGAATTGCTG TTATGTTTTT      250
AAGAAGCTTA TCATAAGTAA TGAGGTTCAT GATTTTTGAC ATAGTTAGCC      300
TCCGCAGTCT TTCATTTCAA GTAAATAATA GCGAAATATT CTTTATACTG      350
AATACTTATA GTGAAGCAAA GTTCTAGCTT TGAGAAAATT CTTTCTGCAA      400
CTAAATATAG TAAATTACGG TAAAATATAA ATAAGTACAT ATTGAAGAAA      450
ATGAGACATA ATATATTTTA TAATAGGAGG                            480
```

2) INFORMATION FOR SEQ ID NO: 19

(i) (A) LENGTH: 458 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: MR108
(C) ACCESSION NUMBER: AB014404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG       50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC      100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA      150
GAAGCATATC ATAAATGATG CGGTTTTTTC AGCCGCTTCA TAAAGGGATT      200
TTGAATGTAT CAGAACATAT GAGGTTTATG TGAATTGCTG TTATGTTTTT      250
AAGAAGCTTA TCATAAGTAA TGAGGTTCAT GATTTTTGAC ATAGTTAGCC      300
TCCGCAGTCT TTCATTTCAA GTAAATAATA GCGAAATATT CTTTATACTG      350
AATACTTATA GTGAAGCAAA GTTCTAGCTT TGAGAAAATT CTTTCTGCAA      400
CTAAATATAG TAAATTACGG TAAAATATAA ATAAGTACAT ATTGAAGAAA      450
ATGAGACA                                                   458
```

2) INFORMATION FOR SEQ ID NO: 20

(i) (A) LENGTH: 385 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/9302
(C) ACCESSION NUMBER: AB014430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG      50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC     100
GGGTTGTGTT AATTGAGCAA GTGTATAGAG CATTTAAGAT TATGCGTGGA     150
GAAGCTTATC ATAAGTAATG AGGTTCATGA TTTTTGACAT AGTTAGCCTC     200
CGCAGTCTTT CATTTCAAGT AAATAATAGC GAAATATTCT TTATACTGAA     250
TACTTATAGT GAAGCAAAGT TCTAGCTTTG AGAAAATTCT TTCTGCAACT     300
AAATATAGTA AATTACGGTA AAATATAAAT AAGTACATAT TGAAGAAAAT     350
GAGACATAAT ATATTTTATA ATAGGAGGGA ATTTC                     385
```

2) INFORMATION FOR SEQ ID NO: 21

(i) (A) LENGTH: 385 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 84/9580
(C) ACCESSION NUMBER: AB014431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG      50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC     100
GGGTTGTGTT AATTGAGCAA GTGTATAGAG CATTTAAGAT TATGCGTGGA     150
GAAGCTTATC ATAAGTAATG AGGTTCATGA TTTTTGACAT AGTTAGCCTC     200
CGCAGTCTTT CATTTCAAGT AAATAATAGC GAAATATTCT TTATACTGAA     250
TACTTATAGT GAAGCAAAGT TCTAGCTTTG AGAAAATTCT TTCTGCAACT     300
AAATATAGTA AATTACGGTA AAATATAAAT AAGTACATAT TGAAGAAAAT     350
GAGACATAAT ATATTTTATA ATAGGAGGGA ATTTC                     385
```

2) INFORMATION FOR SEQ ID NO: 22

(i) (A) LENGTH: 385 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus

(B) STRAIN: 85/1940
(C) ACCESSION NUMBER: AB014432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAGCAA GTGTATAGAG CATTTAAGAT TATGCGTGGA       150
GAAGCTTATC ATAAGTAATG AGGTTCATGA TTTTTGACAT AGTTAGCCTC       200
CGCAGTCTTT CATTTCAAGT AAATAATAGC GAAATATTCT TTATACTGAA       250
TACTTATAGT GAAGCAAAGT TCTAGCTTTG AGAAAATTCT TTCTGCAACT       300
AAATATAGTA AATTACGGTA AAATATAAAT AAGTACATAT TGAAGAAAAT       350
GAGACATAAT ATATTTTATA ATAGGAGGGA ATTTC                       385
```

2) INFORMATION FOR SEQ ID NO: 23

(i) (A) LENGTH: 385 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 61/6219
(C) ACCESSION NUMBER: AB014433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCG CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAAAG CATTTAAGAT TATGCGAGGA       150
GAAGCTTATC ATAAGTAATG AGGTTCATGA TTTTTGACAT AGTTAGCCTC       200
CGCAGTCTTT CATTTCAAGT AAATAATAGC GAAATATTCT TTATACTGAA       250
TACTTATAGT GAAGCAAAGT TCTAGCTTTG AGAAAATTCT TTCTGCAACT       300
AAATATAGTA AATTACGGTA AAATATAAAT AAGTACATAT TGAAGAAAAT       350
GAGACATAAT ATATTTTATA ATAGGAGGGA ATTTC                       385
```

2) INFORMATION FOR SEQ ID NO: 24

(i) (A) LENGTH: 340 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 64/4176
(C) ACCESSION NUMBER: AB014434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

```
CGCAGTAACT ACGCGCTATC ATTCAGCAAA ATGACATTCC CACATCAAAT        50
GATGCGGGTT GTGTTAGTTG AGCAAGTGTA CATAGCATTT AAGATTATGC       100
GAGGAGAAGC TTATCATAAG TAATGAGGTT CATGATTTTT GACATAGTTA       150
GCCTCCGCAG TCTTTCATTT CAAGTAAATA ATAGCGAAAT ATTCTTTATA       200
CTGAATACTT ATAGTGAAGC AAAGTTCTAG CTTTGAGAAA ATTCTTTCTG       250
CAACTAAATA TAGTAAATTA CGGTAAAATA TAAATAAGTA CATATTGAAG       300
AAAATGAGAC ATAATATATT TTATAATAGG AGGGAATTTC                  340
```

2) INFORMATION FOR SEQ ID NO: 25

(i) (A) LENGTH: 369 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 64/3846
(C) ACCESSION NUMBER: AB014435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

```
CAAACGGCCT GCACAAGGAC GTCTTACAAC GCAGTAACTA CGCACTATCA        50
TTCAGCAAAA TGACATTCCC ACATCAAATG ATGCGGGTTG TGTTAATTGA       100
ACAAGTGTAC AGAGCATTTA AGATTATGCG AGGAGAAGCT TATCATAAGT       150
AATGAGGTTC ATGATTTTTG ACATAGTTAG CCTCCGCAGT CTTTCATTTC       200
AAGTAAATAA TAGCGAAATA TTCTTTATAC TGAATACTTA TAGTGAAGCA       250
AAGTTCTAGC TTTGAGAAAA TTCTTTCTGC AACTAAATAT AGTAAATTAC       300
GGTAAAATAT AAATAAGTAC ATATTGAAGA AAATGAGACA TAATATATTT       350
TATAATAGGA GGGAATTTC                                        369
```

2) INFORMATION FOR SEQ ID NO: 26

(i) (A) LENGTH: 3050 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: HUC19
(C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

```
AATTTGGTAA ACCTCAAAAG GTAATTACAG ATCAGGCACC TTCAACGAAG      50
GTAGCAATGG CTAAAGTAAT TAAAGCTTTT AAACTTAAAC CTGACTGTCA     100
TTGTACATCG AAATATCTGA ATAACCTCAT TGAGCAAGAT CACCGTCATA     150
TTAAAGTAAG AAAGACAAGG TATCAAAGTA TCAATACAGC AAAGAATACT     200
TTAAAAGGTA TTGAATGTAT TCACGCTCTA TATAAAAAGA ACCGCAGGTC     250
TCTTCAGATC TACGGATTTT CGCCATGCCA CGAAATTAGC ATCATGCTAG     300
CAAGTTAAGC GAACACTGAC ATGATAAATT AGTGGTTAGC TATATTTTTT     350
TACTTTGCAA CAGAACCGAA AATAATCTCT TCAATTTATT TTTATATGAA     400
TCCTGTGACT CAATGATTGT AATATCTAAA GATTTCAGTT CATCATAGAC     450
AATGTTCTTT TCAACATTTT TTATAGCAAA TTGATTAAAT AAATTCTCTA     500
ATTTCTCCCG TTTGATTTCA CTACCATAGA TTATATTATC ATTGATATAG     550
TCAATGAATA ATGACAAATT ATCACTCATA ACAGTCCCAA CCCCTTTATT     600
TTGATAGACT AATTATCTTC ATCATTGTAA AACAAATTAC ACCCTTTAAA     650
TTTAACTCAA CTTAAATATC GACAAATTAA AAAACAATAA AATTACTTGA     700
ATATTATTCA TAATATATTA ACAACTTTAT TATACTGCTC TTTATATATA     750
AAATCATTAA TAATTAAACA AGCCTTAAAA TATTTAACTT TTTTGTGATT     800
ATTACACATT ATCTTATCTG CTCTTTATCA CCATAAAAAT AGAAAAAACA     850
AGATTCCTAA AGAATATAGG AATCTTGTTT CAGACTGTGG ACAAACTGAT     900
TTTTTATCAG TTAGCTTATT TAGAAAGTTT TATTTAAATT ACAGTTTCTA     950
TTTTTATTAG ATCACAATTT TATTTTAGCT CTTGTTCAAG TAATCATTTT    1000
TCGCCAAAAA CTTTATACTG AATAGCTTCT ACATTAAATA CTTGTCAATG    1050
AGATCATCTA CATCTTTAAA TTCAGAATAA TTCGCATATG GATCTATAAA    1100
ATAAAATTGT GGTTCTTTAC CGGAAACATT AAATATTCTT AATATTAAAT    1150
ATTTCTGCTT ATATTCTTTC ATAGCAAACA TTTCATTTAG CGACATAAAA    1200
AATGGTTCCT CAATACTAGA AGATGTAGAT GTTTTAATTT CAATAAATTT    1250
TTCTACAGCT TTATCTGTAT TTGTTGGATC AAAAGCTACT AAATCATAGC    1300
CATGACCGTG TTGAGAGCCT GGATTATCAT TTAAAATATT CCTAAACTGT    1350
TCTTTCTTAT CTTCGTCTAT TTTATTATCA ATTAGCTCAT TAAAGTAATT    1400
TAGCGCTAAT TTTTCTCCAA CTTTACCGGT TAATTTATTC TCTTTATTTG    1450
ATTTTTCAAT TTCTGAATCA TTTTTAGTAG TCTTTGATAC ACCTTTTTTA    1500
TATTTTGGAA TTATTCCTTT AGGTGCTTCC ACTTCCTTGA GTGTCTTATC    1550
TTTTTGTGCT GTTCTAATTT CTTCAATTTC GCTGTCTTCC TGTATTTCGT    1600
CTATGCTATT GACCAAGCTA TCATAGGATG TTTTTGTAAC TTTTGAAGCT    1650
AATTCATTAA ATAGTTCTAA AAATTTCTTT AAATCCTCTA GCATATCTTC    1700
TTCTGTGAAT CCTTCATTCA AATCATAATA TTTGAATCTT ATTGATCCAT    1750
GAGAATATCC TGATGGATAA TCATTTTTTA AATCATAAGA TGAATCTTTA    1800
TTTTCTGCGT AATAAAATCT TCCAGTATTA AATTCATTTG ATGTAATATA    1850
TTTATTGAGT TCGGAAGATA AAGTTAATGC TCTTTGTTTT GCAGCATTTT    1900
TATCCCGCGG AAACATATCA CTTATCTTTG ACCATCCTTG ATTCAAAGAT    1950
AAGTATATGC CTTCTCCTTC CGGATGAAAA AGATATACCA AATAATGTCC    2000
ATCCTTTGTT TCTTTTGTTA TATTCTCATC ATATATTGAA ATCCAAGGAA    2050
CTTTACTATA GTTCCCAGTA GCAACCTTCC CTACAACTGA ATATTTATCT    2100
TCTTTTATAT GCACTTTTAA CTGCTTGGGT AACTTATCAT GGACTAAAGT    2150
TTTATATAGA TCACCTTTAT CCCAATCAGA TTTTTTAACT ACATTATTGG    2200
```

```
TACGTTTCTC TTTAATTAAT TTAAGGACCT GCATAAAGTT GTCTATCATT      2250
TGAAATTCCC TCCTATTATA AAATATATTA TGTCTCATTT TCTTCAATAT      2300
GTACTTATTT ATATTTTACC GTAATTTACT ATATTTAGTT GCAGAAAGAA      2350
TTTTCTCAAA GCTAGAACTT TGCTTCACTA TAAGTATTCA GTATAAAGAA      2400
TATTTCGCTA TTATTTACTT GAAATGAAAG ACTGCGGAGG CTAACTATGT      2450
CAAAAATCAT GAACCTCATT ACTTATGATA AGCTTCTTAA AAACATAACA      2500
GCAATTCACA TAAACCTCAT ATGTTCTGAT ACATTCAAAA TCCCTTTATG      2550
AAGCGGCTGA AAAAACCGCA TCATTTATGA TATGCTTCTC CTCGCATAAT      2600
CTTAAATGCT CTGTACACTT GTTCAATTAA CACAACCCGC ATCATTTGAT      2650
GTGGGAATGT CATTTTGCTG AATGATAGTG CGTAGTTACT GCGTTGTAAG      2700
ACGTCCTTGT GCAGGCCGTT TGATCCGCCA ATGACGAAAA CAAAGTCGCT      2750
TTGCCCTTGG GTCATGCGTT GGTTCAATTC TTGGGCCAAT CCTTCGGAAG      2800
ATAGCATCTT TCCTTGTATT TCTAATGTAA TGACTGTGGA TTGTGGTTTG      2850
ATTTTGGCTA GTATTCGTTG GCCTTCTTTT TCTTTTACTT GCTCAATTTC      2900
TTTGTCACTC ATATTTTCTG GTGCTTTTTC GTCTGGAACT TCTATGATGT      2950
CTATCTTGGT GTATGGGCCT AAACGTTTTT CATATTCTGC TATGGCTTGC      3000
TTCCAATATT TCTCTTTTAG TTTCCCTACA GCTAAAATGG TGATTTTCAT      3050
```

2) INFORMATION FOR SEQ ID NO: 27

(i) (A) LENGTH: 657 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

```
CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA        50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC       100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT       150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG       200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT       250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA       300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT       350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT       400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA       450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT       500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG       550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT       600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT       650
AAATAAA                                                     657
```

2) INFORMATION FOR SEQ ID NO: 28

(i) (A) LENGTH: 782 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

```
CACCTTCATA TGACGTCTAT CCATTTATGT ATGGCATGAG TAACGAAGAA        50
TATAATAAAT TAACCGAAGA TAAAAAAGAA CCTCTGCTCA ACAAGTTCCA       100
GATTACAACT TCACCAGGTT CAACTCAAAA AATATTAACA GCAATGATTG       150
GGTTAAATAA CAAAACATTA GACGATAAAA CAAGTTATAA AATCGATGGT       200
AAAGGTTGGC AAAAAGATAA ATCTTGGGGT GGTTACAACG TTACAAGATA       250
TGAAGTGGTA AATGGTAATA TCGACTTAAA ACAAGCAATA GAATCATCAG       300
ATAACATTTT CTTTGCTAGA GTAGCACTCG AATTAGGCAG TAAGAAATTT       350
GAAAAAGGCA TGAAAAAACT AGGTGTTGGT GAAGATATAC CAAGTGATTA       400
TCCATTTTAT AATGCTCAAA TTTCAAACAA AAATTTAGAT AATGAAATAT       450
TATTAGCTGA TTCAGGTTAC GGACAAGGTG AAATACTGAT TAACCCAGTA       500
CAGATCCTTT CAATCTATAG CGCATTAGAA AATAATGGCA ATATTAACGC       550
ACCTCACTTA TTAAAAGACA CGAAAAACAA AGTTTGGAAG AAAAATATTA       600
TTTCCAAAGA AAATATCAAT CTATTAACTG ATGGTATGCA ACAAGTCGTA       650
AATAAAACAC ATAAAGAAGA TATTTATAGA TCTTATGCAA ACTTAATTGG       700
CAAATCCGGT ACTGCAGAAC TCAAAATGAA ACAAGGAGAA ACTGGCAGAC       750
AAATTGGGTG GTTTATATCA TATGATAAAG AT                          782
```

2) INFORMATION FOR SEQ ID NO: 29

(i) (A) LENGTH: 744 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

```
TATGACGTCT ATCCATTTAT GTATGGCATG AGTAACGAAG AATATAATAA        50
ATTAACCGAA GATAAAAAAG AACCTCTGCT CAACAAGTTC CAGATTACAA       100
CTTCACCAGG TTCAACTCAA AAAATATTAA CAGCAATGAT TGGGTTAAAT       150
AACAAAACAT TAGACGATAA AACAAGTTAT AAAATCGATG GTAAAGGTTG       200
GCAAAAAGAT AAATCTTGGG GTGGTTACAA CGTTACAAGA TATGAAGTGG       250
TAAATGGTAA TATCGACTTA AAACAAGCAA TAGAATCATC AGATAACATT       300
TTCTTTGCTA GAGTAGCACT CGAATTAGGC AGTAAGAAAT TTGAAAAAGG       350
CATGAAAAAA CTAGGTGTTG GTGAAGATAT ACCAAGTGAT TATCCATTTT       400
```

```
ATAATGCTCA AATTTCAAAC AAAAATTTAG ATAATGAAAT ATTATTAGCT      450
GATTCAGGTT ACGGACAAGG TGAAATACTG ATTAACCCAG TACAGATCCT      500
TTCAATCTAT AGCGCATTAG AAAATAATGG CAATATTAAC GCACCTCACT      550
TATTAAAAGA CACGAAAAAC AAAGTTTGGA AGAAAAATAT TATTTCCAAA      600
GAAAATATCA ATCTATTAAC TGATGGTATG CAACAAGTCG TAAATAAAAC      650
ACATAAAGAA GATATTTATA GATCTTATGC AAACTTAATT GGCAAATCCG      700
GTACTGCAGA ACTCAAAATG AAACAAGGAG AAACTGGCAG ACAA            744
```

2) INFORMATION FOR SEQ ID NO: 30

(i) (A) LENGTH: 652 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

```
CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA       50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC      100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT      150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG      200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT      250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA      300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT      350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT      400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA      450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT      500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG      550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT      600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT      650
AA                                                         652
```

2) INFORMATION FOR SEQ ID NO: 31

(i) (A) LENGTH: 2436 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

```
CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA      50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC     100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT     150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG     200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT     250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA     300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT     350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT     400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA     450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT     500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG     550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT     600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT     650
AAATAAAACA CATAAAGAAG ATATTTATAG ATCTTATGCA AACTTAATTG     700
GCAAATCCGG TACTGCAGAA CTCAAAATGA AACAAGGAGA AACTGGCAGA     750
CAAATTGGGT GGTTTATATC ATATGATAAA GATAATCCAA ACATGATGAT     800
GGCTATTAAT GTTAAAGATG TACAAGATAA AGGAATGGCT AGCTACAATG     850
CCAAAATCTC AGGTAAAGTG TATGATGAGC TATATGAGAA CGGTAATAAA     900
AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC GTAACGATGG     950
TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT TACTTCTCCC    1000
TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG ACACTGTAAC    1050
GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT TCAGCGATAA    1100
CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT AACGTTATTC    1150
ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT CTTCTACCCA    1200
TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA ATGATACCTT    1250
TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT ATATTGAGGA    1300
TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA TATGAAGGCT    1350
TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT TTCATATATG    1400
TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA TGTTAAAGGT    1450
AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT TCTATTGAGA    1500
CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA TCAACTCCCC    1550
AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT CCATACGTTC    1600
AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT TAGTAAGTTT    1650
GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT AAAAGTGTTC    1700
TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC TCTGTTATAT    1750
TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT TAAAGCTTGA    1800
AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT TCTTCCACTT    1850
GCTTAACCAT ACTTTTAGAA AGTGCTAGTC CATTCGGTCC AGTAATACCT    1900
TTTAATTCTA CATTTAAATT CATATTATAT TCATTTGCTA TTTTTACTAC    1950
ATCATCGAAA GTTGGCAAAT GTTCATCTTT GAATTTTTCA CCAAACCAAG    2000
ATCCTGCAGA AGCATCTTTA ATTTCATCAT AATTCAATTC AGTTATTTCC    2050
CCGGACATAT TTGTAGTCCG TTCTAAATAA TCATCATGAA TGATAATCAG    2100
TTGTTCATCT TTTGTAATTG CAACATCTAA CTCCAACCAG TTTATACCTT    2150
CTACTTCTGA AGCAGCTTTA AATGATGCAA TTGTATTTTC CGGAGCTTTA    2200
CTAGGTAATC CTCTATGTCC ATATACAGTT AGCATATTAC CTCTCCTTGC    2250
ATTTTTATTT TTTTAATTAA CGTAACTGTA TTATCACATT AATCGCACTT    2300
TTATTTCCAT TAAAAAGAGA TGAATATCAT AAATAAAGAA GTCGATAGAT    2350
TCGTATTGAT TATGGAGTTA ATCTACGTCT CATCTCATTT TTAAAAAATC    2400
ATTTATGTCC CAAGCTCCAT TTTGTAATCA AGTCTA                   2436
```

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

CGCTTGCCAC ATCAAATGAT GCGGGTTGTG CAAGCG **36**

2) INFORMATION FOR SEQ ID NO: 33

(i) (A) LENGTH: 336 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus epidermidis
(B) STRAIN: G3
(C) ACCESSION NUMBER: SEQ ID NO:15, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

```
CTCATTACTT ATGATAAGCT TCTTAAAAAC ATAACAGCAA TTCACATAAA       50
CCTCATATGT TCTGATACAT TCAAAATCCC TTTATGAAGC GGCTGAAAAA      100
ACCGCATCAT TTATGATATG CTTCGCCTCT CATGATCTTA AATGCGCGAT      150
AAATTTGTTC GATCAATATG ACGCGCATAT TTGGTGTGGG AAGGTCATAT      200
TGCTAAAAGA TAAAGCATAG TTGCTGCGTT GTAAGACGTC TTGGTGTAAA      250
CCATTGGAGC CACCTATGAC AAATGTAAAG TCGCTTTGAC CTTGTGTCAT      300
GCGTGTTTGT AGTTCTTTAG CGAGTCCTTC TGAAGA                     336
```

2) INFORMATION FOR SEQ ID NO: 34

(i) (A) LENGTH: 260 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus haemolyticus
(B) STRAIN: SH 518
(C) ACCESSION NUMBER: SEQ ID NO:16, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

```
CTCATTACTT ATGATAAGCT TCTTAAAAAC ATAACAGCAA TCCACATAAA        50
CCTCATATGT TCTGATACAT TCAAAATCCC TTTATGAAGC GGCTGAAAAA       100
ACCGCATCAT TTATGATATG CTTCCCTCGC ATGATTTTAA ATGCTCTGTA       150
TACTTGCTCG ATTAAGACAA CGCGCATCAT TTGATGTGGG AATGTCATTT       200
TACTGAATGA AAGTGCGTAG TTGCTGCGTT GTAAGACGTC CTCATGCAAT       250
CCATTTGATC                                                  260
```

2) INFORMATION FOR SEQ ID NO: 35

(i) (A) LENGTH: 225 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: ATCC 25923
(C) ACCESSION NUMBER: SEQ ID NO:9, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAGGCGTATC ACAAATAAAA CTAAAAATGG AGTAACTATT AATATAGTAT       200
AAATTCAATA TGGTGATAAA AACAG                                  225
```

2) INFORMATION FOR SEQ ID NO: 36

(i) (A) LENGTH: 225 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: STP23
(C) ACCESSION NUMBER: SEQ ID NO:10 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAGGCGTATC ACAAATAAAA CTAAAAATGG AGTAACTATT AATATAGTAT       200
AAATTCAATA TGGTGATAAA AACAG                                  225
```

2) INFORMATION FOR SEQ ID NO: 37

(i) (A) LENGTH: 225 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: STP43
(C) ACCESSION NUMBER: SEQ ID NO:12 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGTAG        50
TAACTACGCA CTATCATTCA GCAAAATGAC ATTTCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTACAGAG CATTTAAGAT TATGCGTGGA       150
GAGGCGTATC ATAAGTAATG AGGTTCATGA TTTTTGACAT AGTTAGCCTC       200
CGCAGTCTTT CAAGTAAATA ATATC                                  225
```

2) INFORMATION FOR SEQ ID NO: 38

(i) (A) LENGTH: 225 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: STP53
(C) ACCESSION NUMBER: SEQ ID NO:13 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

```
TTCGTCATTG GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG        50
TAACTACGCA CTATCATTTA GCAAAATGAC ATTCCCACAT CAAATGATGC       100
GGGTTGTGTT AATTGAACAA GTGTATAGAG CATTTAAGAT TATGCGTGGA       150
GAGGCGTATC ATAAGTGATG CTTGTTAGAA TGATTTTTAA CAATATGAAA       200
```

TAGCTGTGGA AGCTCAAACA TTTGT 225

2) INFORMATION FOR SEQ ID NO: 39

(i) (A) LENGTH: 1500 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 476
(C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

TGAGTCTGGT AAAGATACAC AACCAATTGG TAAAGAGAAA GTGATGAATC 50
CAGCGAAACA ACCAGCGACA GGTAAAGTTG TGTTGTTACC AGCGCATAGA 100
GGAACTGTTA GTAGCGGTAC AGAAGGTTCT GATCGCGCAT TAGAAGGAAC 150
TGCTGTATCA AGTAAGAGTG GGAAACAATT GGCTAACATG TCAGCGCCTA 200
AAGGTAGCGC ACATGAGAAA CAGTTACCAA AAACTGGAAC TGATCAAAGT 250
TCAAGCCCAG CAGCGATGTT TGTATTAGTA ACAGGTATAG GTTTAATCGC 300
GACTGTACGA CGTAGAAAAG CTAGCTAAAA TATATTGAAA ACAATACTAC 350
TGTATTTCTT AAATAAGAGG TACGGTAGTG TTTTTTTATG GAAAAAAGCT 400
ATAACCGTTG ATAAATATGG GATATAAAAA CGGGGATAAG TAATAAGACA 450
TCAAGGTATT TATCCACAGA AATGGGGATA GTTATCCAGA ATTGTGTACA 500
ATTTAAAGAG AAATACCCAC AATGCCCACA GAGTTATCCA CAAATACACA 550
AGTTATACAC TGAAAATTGG GCATGAATGT CAGAAAAATA TCAAAAACTG 600
CAAAAAAACT TGGTATAATA AGAGGGAAAA GTGTGAACAA GTTAATAACT 650
TGTGGATAAC TGGAAAGTTG ATAACAATTT GGAGGACCAA ACGACATGAA 700
AATCACCATT TTAGcTGTAG GGAAACTAAA AGAGAAATAT TGGAAGCAAG 750
CCATAGCAGA ATATGAAAAA CGTTTAGGCC CATACACCAA GATAGACATC 800
ATAGAAGTTA CAGACGAAAA AGCACCAGAA AATATGAGCG ACAAAGAAAT 850
CGAGCAAGTA AAAGAAAAAG AAGGCCAACG AATACTAGCC AAAATCAAAC 900
CACAATCCAC AGTCATTACA TTAGAAATAC AAGGAAAGAT GCTATCTTCC 950
GAAGGATTGG CCCAAGAATT GAACCAACGC ATGACCCAAG GGCAAAGCGA 1000
CTTTGTATTC GTCATTGGCG GATCAAACGG CCTGCACAAG GACGTCTTAC 1050
AACGTAGTAA CTACGCACTA TCATTCAGCA AAATGACATT TCCACATCAA 1100
ATGATGCGGG TTGTGTTAAT TGAACAAGTG TACAGAGCAT TTAAGATTAT 1150
GCGTGGAGAA GCTTATCATA AATGATGCGG TTTTTTCTTG AAAAATTTAA 1200
TTAGATATTA GAATCCTTTA ATTTATTTGA AAATCAGAAG TGAGTAACAA 1250
TGGTAAGTGA AATAGTTAGT GCAATAATTG GAATTATAGG GATTTATTGA 1300
GATGTATGGA GATGCGGGGC ATTTATCGAG TAGATTACAA TTAGAGCATG 1350
TAGGTGATTT GCTTTTTCAT GCAAGTAAAG ATAAACTTTT AAAAATCCTA 1400
TAAGAATTTA GAAACTTTAG AATAACTAAA TATTAAAAAA ATATCGTATG 1450
AAAGTGAAAT TAGGATGAGA GACCATAGCT AAATTAAAAA TTTTAGCAAA 1500

2) INFORMATION FOR SEQ ID NO: 40

(i) (A) LENGTH: 1501 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 252
(C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

```
TTGCACAACC AATTGGTAAA GACAAAGTGA TGGATCCAGC GAAACAACCA        50
GCGCCAAGTA AAGTTGTATT GTTGCCAGCG CATAGAGGAA CTGTTAGTAG       100
TGGTAGAGAA GGTTCTGATC GCGCATTGGA AGGAACTGCT GTATCAAGTA       150
AGAGCGGGAA ACAATTGGCT AGCATGTCAG CGCCTAAAGG TAGCACACAT       200
GAGAAGCAGT TACCAAAAAC TGGAACTGAT CAAAGTTCAA GCCCAGCAGC       250
GATGTTTGTA TTAGTAGCAG GTATAGGTTT AATTGCGACT GTACGACGTA       300
GAAAAGCTAG CTAAAATATA TTGAAAACAA TACTACTGTA TTTCTTAAAC       350
AAGAGGTACG GTAGTGTTTT TTTATGAAAA AAAGCTATAA CCGTTGATAA       400
ATATGGGATA TAAAAACGGG GATAAGTAAT AAGACATCAA GGTATTTATC       450
CACAGAAATG GGGATAGTTA TCCAGAATTG TGTACAATTT AAAGAGAAAT       500
ACCCACAATG CCCACAGAGT TATCCACAAA TACACAGGTT ATACACTAAA       550
AATTGGGCAT GAATGTCAGA AAAATATCAA AAACTGCAAA GAATATTGGT       600
ATAATAAGAG GGAACAGTGT GAACAAGTTA ATAACTTGTG GATAACTGGA       650
AAGTTGATAA CAATTTGGAG GACCAAACGA CATGAAAATC ACCATTTTAG       700
CTGTAGGGAA ACTAAAAGAG AAATATTGGA AGCAAGCCAT AGCAGAATAT       750
GAAAAACGTT TAGGCCCATA CACCAAGATA GACATCATAG AAGTTCCAGA       800
CGAAAAAGCA CCAGAAAATA TGAGCGACAA AGAAATTGAG CAAGTAAAAG       850
AAAAAGAAGG CCAACGAATA CTAGCCAAAA TCAAACCACA ATCAACAGTC       900
ATTACATTAG AAATACAAGG AAAGATGCTA TCTTCCGAAG GATTGGCCCA       950
AGAATTGAAC CAACGCATGA CCCAAGGGCA AAGCGACTTT GTATTCGTCA      1000
TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG CAGTAACTAC      1050
GCACTATCAT TCAGCAAAAT GACATTCCCA CATCAAATGA TGCGGGTTGT      1100
GTTAATTGAA CAAGTGTACA GAGCATTTAA GATTATGCGT GGAGAAGCAT      1150
ATCATAAATG ATGCGGTTTT TTCAGCCGCT TCATAAAGGG ATTTTGAATG      1200
TATCAGAACA TATGAGGTTT ATGTGAATTG CTGTTATGTT TTTAAGAAGC      1250
TTATCATAAG TAATGAGGTT CATGATTTTT GACATAGTTA GCCTCCGCAG      1300
TCTTTCATTT CAAGTAAATA ATAGCGAAAT ATTCTTTATA CTGAATACTT      1350
ATAGTGAAGC AAAGTTCTAG CTTTGAGAAA ATTCTTTCTG CAACTAAATA      1400
TAGTAAATTA CGGTAAAATA TAAATAAGTA CATATTGAAG AAAATGAGAC      1450
ATAATATATT TTATAATAGG AGGGAATTTC AAATGATAGA CAACTTTATG      1500
C                                                          1501
```

2) INFORMATION FOR SEQ ID NO: 41

(i) (A) LENGTH: 2480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: COL
(C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

```
AAACCGTCTG GCAAACGAAT TAATGCTATT CAAATTTTAA ATAAAGAGAC      50
AGGTAAGTTT GAAAATATTG ATTTAAAACG TGTATATCAC GTAACGATGA     100
ATGACTTCAC AGCATCAGGT GGCGACGGAT ATAGTATGTT CGGTGGTCCT     150
AGAGAAGAAG GTATTTCATT AGATCAAGTA CTAGCAAGTT ATTTAAAAAC     200
AGCTAACTTA GCTAAGTATG ATACGACAGA ACCACAACGT ATGTTATTAG     250
GTAAACCAGC AGTAAGTGAA CAACCAGCTA AAGGACAACA AGGTAGCAAA     300
GGTAGTAAGT CTGGTAAAGA TACACAACCA ATTGGTGACG ACAAAGTGAT     350
GGATCCAGCG AAAAAACCAG CTCCAGGTAA AGTTGTATTG TTGCTAGCGC     400
ATAGAGGAAC TGTTAGTAGC GGTACAGAAG GTTCTGGTCG CACAATAGAA     450
GGAGCTACTG TATCAAGCAA GAGTGGGAAA CAATTGGCTA GAATGTCAGT     500
GCCTAAAGGT AGCGCGCATG AGAAACAGTT ACCAAAAACT GGAACTAATC     550
AAAGTTCAAG CCCAGAAGCG ATGTTTGTAT TATTAGCAGG TATAGGTTTA     600
ATCGCGACTG TACGACGTAG AAAAGCTAGC TAAAATATAT TGAAAATAAT     650
ACTACTGTAT TTCTTAAATA AGAGGTACGG TAGTGTTTTT TTATGAAAAA     700
AAGCGATAAC CGTTGATAAA TATGGGATAT AAAAACGAGG ATAAGTAATA     750
AGACATCAAG GTGTTTATCC ACAGAAATGG GGATAGTTAT CCAGAATTGT     800
GTACAATTTA AAGAGAAATA CCCACAATGC CCACAGAGTT ACCCACAAAT     850
ACACAGGTTA TACACTAAAA ATCGGGCATA AATGTCAGGA AAATATCAAA     900
AACTGCAAAA AATATTGGTA TAATAAGAGG GAACAGTGTG AACAAGTTAA     950
TAACTTGTGG ATAACTGGAA AGTTGATAAC AATTTGGAGG ACCAAACGAC    1000
ATGAAAATCA CCATTTTAGC TGTAGGGAAA CTAAAAGAGA AATATTGGAA    1050
GCAAGCCATA GCAGAATATG AAAAACGTTT AGGCCCATAC ACCAAGATAG    1100
ACATCATAGA AGTTCCAGAC GAAAAAGCAC CAGAAAATAT GAGTGACAAA    1150
GAAATTGAGC AAGTAAAAGA AAAAGAAGGC CAACGAATAC TAGCCAAAAT    1200
CAAACCACAA TCCACAGTCA TTACATTAGA AATACAAGGA AAGATGCTAT    1250
CTTCCGAAGG ATTGGCCCAA GAATTGAACC AACGCATGAC CCAAGGGCAA    1300
AGCGACTTTG TTTTCGTCAT TGGCGGATCA AACGGCCTGC ACAAGGACGT    1350
CTTACAACGC AGTAACTACG CACTATCATT CAGCAAAATG ACATTCCCAC    1400
ATCAAATGAT GCGGGTTGTG TTAATTGAAC AAGTGTACAG AGCATTTAAG    1450
ATTATGCGAG GAGAAGCTTA TCATAAGTAA TGAGGTTCAT GATTTTTGAC    1500
ATAGTTAGCC TCCGCAGTCT TTCATTTCAA GTAAATAATA GCGAAATATT    1550
CTTTATACTG AATACTTATA GTGAAGCAAA GTTCTAGCTT TGAGAAAATT    1600
CTTTCTGCAA CTAAATATAG TAAATTACGG TAAAATATAA ATAAGTACAT    1650
ATTGAAGAAA ATGAGACATA ATATATTTTA TAATAGGAGG GAATTTCAAA    1700
TGATAGACAA CTTTATGCAG GTCCTTAAAT TAATTAAAGA GAAACGTACC    1750
AATAATGTAG TTAAAAAATC TGATTGGGAT AAAGGTGATC TATATAAAAC    1800
TTTAGTCCAT GATAAGTTAC CCAAGCAGTT AAAAGTGCAT ATAAAAGAAG    1850
```

```
ATAAATATTC AGTTGTAGGG AAGGTTGCTA CTGGGAACTA TAGTAAAGTT      1900
CCTTGGATTT CAATATATGA TGAGAATATA ACAAAAGAAA CAAAGGATGG      1950
ATATTATTTG GTATATCTTT TTCATCCGGA AGGAGAAGGC ATATACTTAT      2000
CTTTGAATCA AGGATGGTCA AAGATAAGTG ATATGTTTCC GCGGGATAAA      2050
AATGCTGCAA AACAAAGAGC ATTAACTTTA TCTTCCGAAC TCAATAAATA      2100
TATTACATCA AATGAATTTA ATACTGGAAG ATTTTATTAC GCAGAAAATA      2150
AAGATTCATC TTATGATTTA AAAAATGATT ATCCATCAGG ATATTCTCAT      2200
GGATCAATAA GATTCAAATA TTATGATTTG AATGAAGGAT TCACAGAAGA      2250
AGATATGCTA GAGGATTTAA AGAAATTTTT AGAACTATTT AATGAATTAG      2300
CTTCAAAAGT TACAAAAACA TCCTATGATA GCTTGGTCAA TAGCATAGAC      2350
GAAATACAGG AAGACAGCGA AATTGAAGAA ATTAGAACAG CACAAAAAGA      2400
TAAGACACTC AAGGAAGTGG AAGCACCTAA AGGAATAATT CCAAAATATA      2450
AAAAAGGTGT ATCAAAGACT ACTAAAAATG                            2480
```

2) INFORMATION FOR SEQ ID NO: 42

(i) (A) LENGTH: 1045 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: ATCC 33592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

```
CCAGTTTTTT GTTTAATGAA CAAGGTAAAT TACGAGATAA TATTTGAAGA        50
AAACAATAAA GTAGAGATGG ATTTCCATAT CCTCTTTAGT AGCGGTTTTT       100
ATCTGTAAGG TTTATTAATA ATTAAATAAA TAGGCGGGAT AGTTATATAT       150
AGCTTATTAA TGAAAGAATA TGATTATTAA TTTAGTATTA TATTTTAATA       200
TTAAAAAGAA GATATGAAAT AATTATTCAT ACCTTCCACC TTACAATAAT       250
TAGTTTTCAA TCGAATATTA AGATTATTAG TAGTCTTAAA AGTTAAGACT       300
TCCTTATATT AATGACCTAA TTTATTATTT GCCTCATGAA TTATCTTTTT       350
ATTTCTTTGA TATGTCCCAA ACCACATCGT GATATACACT ACAATAAATA       400
TTATGATGAA ACTAATAATA TTCTCAAAGT TCAGATGGAA CCAACCTGCT       450
AGAATAGCGA GTGGGAAGAA TAGGATTATC ATCAATATAA AGTGAACTAC       500
AGTCTGTTTT GTTATACTCC AATCGGTATC TGTAAATATC AAATTACCAT       550
AAGTAAACAA AATTCCAATC AATGCCCATA GTGCTACACA TATTAGCATA       600
ATAACCGCTT CATTAAAGTT TTCATAATAA ATTTTACCCA TAAAAGAATC       650
TGGATATAGT GGTACATATT TATCCCTTGA AAAAAATAAG TGAAGTAATG       700
ACAGAAATCA TAAGACCAGT GAACGCACCT TTTTGAACAG CGTGGAATAA       750
TTTTTTCATA GTGAGATGGA CCATTCCATT TGTTTCTAAC TTCAAGTGAT       800
CAATGTAATT TAGATTGATA ATTTCTGATT TTGAAATACG CACGAATATT       850
GAACCGACAA GCTCTTCAAT TTGGTAAAGT CGCTGATAAA GTTTTAAAGC       900
TTTATTATTC ATTGTTATCG CATACCTGTT TATCTTCTAC TATGAACTGT       950
GCAATTTGTT CTAGATCAAT TGGGTAAACA TGATGGTTCT GTTGCAAAGT      1000
AAAAAAATAT AGCTAACCAC TAATTTATCA TGTCAGTGTT CGCTT           1045
```

2)INFORMATION FOR SEQ ID NO: 43

(i) (A) LENGTH: 1118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-8895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

```
CAGAGCATTT AAGATTATGC GTGGAGAAGC GTACCACAAA TGATGCGGTT        50
TTTTATCCAG TTTTTTGTTT AATGAACAAG GTAAATTACG AGATAATATT       100
TGAAGAAAAC AATAAAGTAG AGATGGATTT CCATATCCTC TTTAGTAGCG       150
GTTTTTATCT GTAAGGTTTA TTAATAATTA AATAAATAGG CGGGATAGTT       200
ATATATAGCT TATTAATGAA AGAATATGAT TATTAATTTA GTATTATATT       250
TTAATATTAA AAAGAAGATA TGAAATAATT ATTCATACCT TCCACCTTAC       300
AATAATTAGT TTTCAATCGA ATATTAAGAT TATTAGTAGT CTTAAAAGTT       350
AAGACTTCCT TATATTAATG ACCTAATTTA TTATTTGCCT CATGAATTAT       400
CTTTTTATTT CTTTGATATG TCCCAAACCA CATCGTGATA TACACTACAA       450
TAAATATTAT GATGAAACTA ATAATATTCT CAAAGTTCAG ATGGAACCAA       500
CCTGCTAGAA TAGCGAGTGG GAAGAATAGG ATTATCATCA ATATAAAGTG       550
AACTACAGTC TGTTTTGTTA TACTCCAATC GGTATCTGTA AATATCAAAT       600
TACCATAAGT AAACAAAATT CCAATCAATG CCCATAGTGC TACACATATT       650
AGCATAATAA CCGCTTCATT AAAGTTTTCA TAATAAATTT TACCCATAAA       700
AGAATCTGGA TATAGTAGTA CATATTTATC CCTTGAAAAA AATAAGTGAA       750
GTAATGACAG AAATCATAAG ACCAGTGAAC GCACCTTTTT GAACAGCGTG       800
GAATAATTTT TTCATAGTGA GATGGACCAT TCCATTTGTT TCTAACTTCA       850
AGTGATCAAT GTAATTTAGA TTGATAATTT CTGATTTTGA AATACGCACG       900
AATATTGAAC CGACAAGCTC TTCAATTTGG TAAAGTCGCT GATAAAGTTT       950
TAAAGCTTTA TTATTCATTG TTATCGCATA CCTGTTTATC TTCTACTATG      1000
AACTGTGCAA TTTGTTCTAG ATCAATTGGG TAAACATGAT GGTTCTGTTG      1050
CAAAGTAAAA AAATATAGCT AACCACTAAT TTATCATGTC AGTGTTCGCT      1100
TAACTTGCTA GCATGATG                                        1118
```

2)INFORMATION FOR SEQ ID NO: 44

(i) (A) LENGTH: 1118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-8903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```
CAGAGCATTT AAGATTATGC GTGGAGAAGC GTACCACAAA TGATGCGGTT        50
TTTTATCCAG TTTTTTGTTT AATGAACAAG GTAAATTACG AGATAATATT       100
TGAAGAAAAC AATAAAGTAG AGATGGATTT CCATATCCTC TTTAGTAGCG       150
GTTTTTATCT GTAAGGTTTA TTAATAATTA AATAAATAGG CGGGATAGTT       200
ATATATAGCT TATTAATGAA AGAATATGAT TATTAATTTA GTATTATATT       250
TTAATATTAA AAAGAAGATA TGAAATAATT ATTCATACCT TCCACCTTAC       300
AATAATTAGT TTTCAATCGA ATATTAAGAT TATTAGTAGT CTTAAAAGTT       350
AAGACTTCCT TATATTAATG ACCTAATTTA TTATTTGCCT CATGAATTAT       400
CTTTTTATTT CTTTGATATG TCCCAAACCA CATCGTGATA TACACTACAA       450
TAAATATTAT GATGAAACTA ATAATATTCT CAAAGTTCAG ATGGAACCAA       500
CCTGCTAGAA TAGCGAGTGG GAAGAATAGG ATTATCATCA ATATAAAGTG       550
AACTACAGTC TGTTTTGTTA TACTCCAATC GGTATCTGTA AATATCAAAT       600
TACCATAAGT AAACAAAATT CCAATCAATG CCCATAGTGC TACACATATT       650
AGCATAATAA CCGCTTCATT AAAGTTTTCA TAATAAATTT TACCCATAAA       700
AGAATCTGGA TATAGTAGTA CATATTTATC CCTTGAAAAA AATAAGTGAA       750
GTAATGACAG AAATCATAAG ACCAGTGAAC GCACCTTTTT GAACAGCGTG       800
GAATAATTTT TTCATAGTGA GATGGACCAT TCCATTTGTT TCTAACTTCA       850
AGTGATCAAT GTAATTTAGA TTGATAATTT CTGATTTTGA AATACGCACG       900
AATATTGAAC CGACAAGCTC TTCAATTTGG TAAAGTCGCT GATAAAGTTT       950
TAAAGCTTTA TTATTCATTG TTATCGCATA CCTGTTTATC TTCTACTATG      1000
AACTGTGCAA TTTGTTCTAG ATCAATTGGG TAAACATGAT GGTTCTGTTG      1050
CAAAGTAAAA AAATATAGCT AACCACTAAT TTATCATGTC AGTGTTCGCT      1100
TAACTTGCTA GCATGATG                                        1118
```

2) INFORMATION FOR SEQ ID NO: 45

(i) (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

```
AGCATTTAAG ATTATGCGTG GAGAAGCGTA CCACAAATGA TGCGGTTTTT        50
TATCCAGTTT TTTGTTTAAT GAACAAGGTA AATTACGAGA TAATATTTGA       100
AGAAAACAAT AAAGTAGAGA TGGATTTCCA TATCCTCTTT AGTAGCGGTT       150
TTTATCTGTA AGGTTTATTA ATAATTAAAT AAATAGGCGG GATAGTTATA       200
TATAGCTTAT TAATGAAAGA ATATGATTAT TAATTTAGTA TTATATTTTA       250
ATATTAAAAA GAAGATATGA AATAATTATT CATACCTTCC ACCTTACAAT       300
AATTAGTTTT CAATCGAATA TTAAGATTAT TAGTAGTCTT AAAAGTTAAG       350
ACTTCCTTAT ATTAATGACC TAATTTATTA TTTGCCTCAT GAATTATCTT       400
TTTATTTCTT TGATATGTCC CAAACCACAT CGTGATATAC ACTACAATAA       450
ATATTATGAT GAAACTAATA ATATTCTCAA AGTTCAGATG GAACCAACCT       500
GCTAGAATAG CGAGTGGGAA GAATAGGATT ATCATCAATA TAAAGTGAAC       550
TACAGTCTGT TTTGTTATAC TCCAATCGGT ATCTGTAAAT ATCAAATTAC       600
CATAAGTAAA CAAAATTCCA ATCAATGCCC ATAGTGCTAC ACATATTAGC       650
ATAATAACCG CTTCATTAAA GTTTTCATAA TAAATTTTAC CCATAAAAGA       700
ATCTGGATAT AGTGGTACAT ATTTATCCCT TGAAAAAAAT AAGTGAAGTA       750
```

```
ATGACAGAAA TCATAAGACC AGTGAACGCA CCTTTTTGAA CAGCGTGGAA      800
TAATTTTTTC ATAGTGAGAT GGACCATTCC ATTTGTTTCT AACTTCAAGT      850
GATCAATGTA ATTTAGATTG ATAATTTCTG ATTTTGAAAT ACGCACGAAT      900
ATTGAACCGA CAAGCTCTTC AATTTGGTAA AGTCGCTGAT AAAGTTTTAA      950
AGCTTTATTA TTCATTGTTA TCGCATACCT GTTTATCTTC TACTATGAAC     1000
TGTGCAATTT GTTCTAGATC AATTGGGTAA ACATGATGGT TCTGTTGCAA     1050
AGTAAAAAAA TATAGCTAAC CACTAATTTA TCATGTCAGT GTTCGCTTAA     1100
CTTGCTAGCA TGA                                            1113
```

2) INFORMATION FOR SEQ ID NO: 46

(i) (A) LENGTH: 2153 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

```
CTGTAGGGAA ACTAAAAGAG AAATACTGGA AGCAAGCCAT AGCAGAATAT       50
GAAAAACGTT TAGGCCCATA CACCAAGATA GACATCATAG AAGTTCCAGA      100
CGAAAAAGCA CCAGAAAATA TGAGCGACAA AGAAATCGAG CAAGTAAAAG      150
AAAAAGAAGG CCAACGAATA CTAGCCAAAA TCAAACCACA ATCCACAGTC      200
ATTACATTAG AAATACAAGG AAAGATGCTA TCTTCCGAAG GATTGGCCCA      250
AGAATTGAAC CAACGCATGA CCCAAGGGCA AAGCGACTTT GTATTCGTCA      300
TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG CAGTAACTAC      350
GCACTATCAT TCAGCAAAAT GACATTCCCA CATCAAATGA TGCGGGTTGT      400
GTTAATTGAA CAAGTGTACA GAGCATTTAA GATTATGCGT GGAGAAGCGT      450
ACCACAAATG ATGCGGTTTT TTATCCAGTT TTTTGTTTAA TGAACAAGGT      500
AAATTACGAG ATAATATTTG AAGAAAACAA TAAAGTAGAG ATGGATTTCC      550
ATATCCTCTT TAGTAGCGGT TTTTATCTGT AAGGTTTATT AATAATTAAA      600
TAAATAGGCG GGATAGTTAT ATATAGCTTA TTAATGAAAG AATATGATTA      650
TTAATTTAGT ATTATATTTT AATATTAAAA AGAAGATATG AAATAATTAT      700
TCATACCTTC CACCTTACAA TAATTAGTTT TCAATCGAAT ATTAAGATTA      750
TTAGTAGTCT TAAAAGTTAA GACTTCCTTA TATTAATGAC CTAATTTATT      800
ATTTGCCTCA TGAATTATCT TTTTATTTCT TTGATATGTC CCAAACCACA      850
TCGTGATATA CACTACAATA AATATTATGA TGAAACTAAT AATATTCTCA      900
AAGTTCAGAT GGAACCAACC TGCTAGAATA GCGAGTGGGA AGAATAGGAT      950
TATCATCAAT ATAAAGTGAA CTACAGTCTG TTTTGTTATA CTCCAATCGG     1000
TATCTGTAAA TATCAAATTA CCATAAGTAA ACAAAATTCC AATCAATGCC     1050
CATAGTGCTA CACATATTAG CATAATAACC GCTTCATTAA AGTTTTCATA     1100
ATAAATTTTA CCCATAAAAG AATCTGGATA TAGTGGTACA TATTTATCCC     1150
TTGAAAAAAA TAAGTGAAGT AATGACAGAA ATCATAAGAC CAGTGAACGC     1200
ACCTTTTTGA ACAGCGTGGA ATAATTTTTT CATAGTGAGA TGGACCATTC     1250
CATTTGTTTC TAACTTCAAG TGATCAATGT AATTTAGATT GATAATTTCT     1300
GATTTTGAAA TACGCACGAA TATTGAACCG ACAAGCTCTT CAATTTGGTA     1350
AAGTCGCTGA TAAAGTTTTA AAGCTTTATT ATTCATTGTT ATCGCATACC     1400
TGTTTATCTT CTACTATGAA CTGTGCAATT TGTTCTAGAT CAATTGGGTA     1450
AACATGATGG TTCTGTTGCA AAGTAAAAAA ATATAGCTAA CCACTAATTT     1500
ATCATGTCAG TGTTCGCTTA ACTTGCTAGC ATGATGCTAA TTTCGTGGCA     1550
```

```
TGGCGAAAAT CCGTAGATCT GATGAGACCT GCGGTTCTTT TTATATAGAG      1600
CGTAAATACA TTCAATACCT TTTAAAGTAT TCTTTGCTGT ATTGATACTT      1650
TGATACCTTG TCTTTCTTAC TTTAATATGA CGGTGATCTT GCTCAATGAG      1700
GTTATTCAAA TATTTCGATG TACAATGACA GTCAGGTTTA AGTTTAAAAG      1750
CTTTAATTAC TTTAGCCATT GCTACCTTCG TTGAAGGTGC CTGATCTGTA      1800
ATTACCTTTT GAGGTTTACC AAATTGTTTA ATGAGACGTT TAATAAACGC      1850
ATATGCTGAA TGATTATCTC GTTGCTTACG CAACCAAATA TCTAATGTAT      1900
GTCCCTCTGC ATCAATGGCA CGATATAAAT AGCTCCATTT TCCTTTTATT      1950
TTGATGTACG TCTCATCAAT ACGCCATTTG TAATAAGCTT TTTTATGCTT      2000
TTTCTTCCAA ATTTGATATA AAATTGGGGC ATATTCTTGA ACCCAACGGT      2050
AGACCGTTGA ATGATGAACG TTTACACCAC GTCCCCTTAA TATTTCAGAT      2100
ATATCACGAT AACTCAATGC ATATCTTAGA TAGTAGCCAA CGGCTACAGT      2150
GAT                                                        2153
```

2) INFORMATION FOR SEQ ID NO: 47

(i) (A) LENGTH: 737 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

```
TTTAAGATTA TGCGTGGAGA AGCATATCAT AAATGATGCG GTTATTTCAG       50
CCGTAATTTT ATAATATAAA GCAGAGTTTA TTAAATTTTA ATGATTACTT      100
TTTATTAAGA ATTAATTCTA GTTGATATAT TATAATGTGA AACACAAAAT      150
AATAATTTGT AATTGTTAGT TTATAGGCAT CTGTATTTGG AATTTTTTGT      200
AGACTATTTA AAAAATAGTG TATATAAGTA TTGAGTTCAT GTATTAACTG      250
TCTTTTTTCA TCGTTCATCA AGTATAAGGA TGTAGAGATT TGTTGGATAA      300
TTTCTTCGGA TGTTTTTAAA ATTATCATTA AATTAGATGG TATCTGATCT      350
TGAGTTTTGT TTTTAGTGTA TGTATATTTT AAAAAATTTT TGATTGTTGT      400
TATTTGACTC TCTTTTAATT TGACACCCTC ATCAATAAAT GTGTTAAATA      450
TATCTTCATT TGTACTTAAA TCATCAAAAT TTGCCAACAA ATATTTGAAC      500
GTCTCTAAAT CATTATGTTT GAGTTCCGTT TTGCTATTCC ATAATTCCAA      550
ACCATTTGGT AGAAAGCCCA AGCTGTGATT TTGATCTCCC CATATAGCTG      600
AATTTAAATC AGTGAGTTGA TTAATTTTTT CAACACAGAA ATGTAATTTT      650
GGAATGAGGA ATCGAAGTTG TTCTTCTACT TGCTGTACTT TTCTTTTGTT      700
TTCAATAAAA TTTCTACACC ATACTGTTAT CAAACCG                    737
```

2) INFORMATION FOR SEQ ID NO: 48

(i) (A) LENGTH: 1592 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

```
AACTAAAAGA GAAATATTGG AAGCAAGCCA TAGCAGAATA TGAAAAACGT        50
TTAGGCCCAT ACACCAAGAT AGACATCATA GAAGTTCCAG ACGAAAAAGC       100
ACCAGAAAAT ATGAGTGACA AAGAAATTGA GCAAGTAAAA GAAAAAGAAG       150
GCCAACGAAT ACTAGCCAAA ATCAAACCAC AATCCACAGT CATTACATTA       200
GAAATACAAG GAAAGATGCT ATCTTCCGAA GGATTGGCCC AAGAATTGAA       250
CCAACGCATG ACCCAAGGGC AAAGCGACTT TGTTTTCGTC ATTGGCGGAT       300
CAAACGGCCT GCACAAGGAC GTCTTACAAC GCAGTAACTA CGCACTATCA       350
TTCAGCAAAA TGACATTCCC ACATCAAATG ATGCGGGTTG TGTTAATTGA       400
ACAAGTGTAC AGAGCATTTA AGATTATGCG AGGAGAAGCA TATCATAAAT       450
GATGCGGTTA TTTCAGCCGT AATTTTATAA TATAAAGCAG AGTTTATTAA       500
ATTTTAATGA TTACTTTTTA TTAAGAATTA ATTCTAGTTG ATATATTATA       550
ATGTGAAACA CAAAATAATA ATTTGTAATT GTTAGTTTAT AGGCATCTGT       600
ATTTGGAATT TTTTGTAGAC TATTTAAAAA ATAGTGTATA TAAGTATTGA       650
GTTCATGTAT TAACTGTCTT TTTTCATCGT TCATCAAGTA TAAGGATGTA       700
GAGATTTGTT GGATAATTTC TTCGGATGTT TTTAAAATTA TCATTAAATT       750
AGATGGTATC TGATCTTGAG TTTTGTTTTT AGTGTATGTA TATTTTAAAA       800
AATTTTTGAT TGTTGTTATT TGACTCTCTT TTAATTTGAC ACCCTCATCA       850
ATAAATGTGT TAAATATATC TTCATTTGTA CTTAAATCAT CAAAATTTGC       900
CAACAAATAT TTGAACGTCT CTAAATCATT ATGTTTGAGT TCCGTTTTGC       950
TATTCCATAA TTCCAAACCA TTTGGTAGAA AGCCCAAGCT GTGATTTTGA      1000
TCTCCCCATA TAGCTGAATT TAAATCAGTG AGTTGATTAA TTTTTTCAAC      1050
ACAGAAATGT AATTTTGGAA TGAGGAATCG AAGTTGTTCT TCTACTTGCT      1100
GTACTTTTCT TTTGTTTTCA ATAAAATTTC TACACCATAC TGTTATCAAA      1150
CCGCCAATTA TTGTGCACAA TCCTCCAATG ATTGTAGATA AAATTGACAA      1200
TATATTACAC ACCTTTCTTA GAGGTTTATT AACATCTATT TTTGAATTTA      1250
AAATTATTAC TTTGGTAGCG TTATAACCTA TTTAACAGAT TAGAGAAAAA      1300
TTGAATGATC GATTGAAGAA TTTCCAAAAT ACCGTCCCAT ATGCGTTGAA      1350
GGAGATTTCT ATTTTCTTCT GTATTCAAAT CTTTGGCTTT ATCCTTTGCT      1400
TTATTCAATA AATCATCTGA GTTTTTTTCA ATATTTTTTA ATACATCTTT      1450
GGCATTTTGT TTAAATACTT TAGGATCGGA AGTTAGGGCA TTAGAGTTTG      1500
CCACATTAAT CATATTATTA TTAATCATTT GAATTTGATT ATCTGATAAT      1550
ATCTCTGATA ACCTACGCTC ATCGAGGACT TTATTAACAG TG              1592
```

2) INFORMATION FOR SEQ ID NO: 49

(i) (A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

```
AGCATTTAAG ATTATGCGTG GAGAAGCATA TCATAAATGA TGCGGTTATT        50
TCAGCCGTAA TTTTATAATA TAAAGCAGAG TTTATTAAAT TTTAATGATT       100
ACTTTTTATT AAGAATTAAT TCTAGTTGAT ATATTATAAT GTGAAACACA       150
AAATAATAAT TTGTAATTGT TAGTTTATAG GCATCTGTAT TTGGAATTTT       200
TTGTAGACTA TTTAAAAAAT AGTGTATATA AGTATTGAGT TCATGTATTA       250
ACTGTCTTTT TTCATCGTTC ATCAAGTATA AGGATGTAGA GATTTGTTGG       300
ATAATTTCTT CGGATGTTTT TAAAATTATC ATTAAATTAG ATGGTATCTG       350
ATCTTGAGTT TTGTTTTTAG TGTATGTATA TTTTAAAAAA TTTTTGATTG       400
TTGTTATTTG ACTCTCTTTT AATTTGACAC CCTCATCAAT AAATGTGTTA       450
AATATATCTT CATTTGTACT TAAATCATCA AAATTTGCCA ACAAATATTT       500
GAACGTCTCT AAATCATTAT GTTTGAGTTC CGTTTTGCTA TTCCATAATT       550
CCAAACCATT TGGTAGAAAG CCCAAGCTGT GATTTTGATC TCCCCATATA       600
GCTGAATTTA AATCAGTGAG TTGATTAATT TTTTCAACAC AGAAATGTAA       650
TTTTGGAATG AGGAATCGAA GTTGTTCTTC TACTTGCTGT ACTTTTCTTT       700
TGTTTTCAAT AAAATTTCTA CACCATACTG                             730
```

2) INFORMATION FOR SEQ ID NO: 50

(i) (A) LENGTH: 1696 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

```
AAAGAGAAAT ATTGGAAGCA AGCCATAGCA GAATATGAAA AACGTTTAGG        50
CCCATACACC AAGATAGACA TCATAGAAGT TCCAGACGAA AAAGCACCAG       100
AAAATATGAG TGACAAAGAA ATTGAGCAAG TAAAAGAAAA AGAAGGCCAA       150
CGAATACTAG CCAAAATCAA ACCACAATCC ACAGTCATTA CATTAGAAAT       200
ACAAGGAAAG ATGCTATCTT CCGAAGGATT GGCCCAAGAA TTGAACCAAC       250
GCATGACCCA AGGGCAAAGC GACTTTGTTT TCGTCATTGG CGGATCAAAC       300
GGCCTGCACA AGGACGTCTT ACAACGCAGT AACTACGCAC TATCATTCAG       350
CAAAATGACA TTCCCACATC AAATGATGCG GGTTGTGTTA ATTGAACAAG       400
TGTACAGAGC ATTTAAGATT ATGCGAGGAG AAGCATATCA TAAATGATGC       450
GGTTATTTCA GCCGTAATTT TATAATATAA AGCAGAGTTT ATTAAATTTT       500
AATGATTACT TTTTATTAAG AATTAATTCT AGTTGATATA TTATAATGTG       550
AAACACAAAA TAATAATTTG TAATTGTTAG TTTATAGGCA TCTGTATTTG       600
GAATTTTTTG TAGACTATTT AAAAAATAGT GTATATAAGT ATTGAGTTCA       650
TGTATTAACT GTCTTTTTTC ATCGTTCATC AAGTATAAGG ATGTAGAGAT       700
TTGTTGGATA ATTTCTTCGG ATGTTTTTAA AATTATCATT AAATTAGATG       750
GTATCTGATC TTGAGTTTTG TTTTTAGTGT ATGTATATTT TAAAAAATTT       800
TTGATTGTTG TTATTTGACT CTCTTTTAAT TTGACACCCT CATCAATAAA       850
TGTGTTAAAT ATATCTTCAT TTGTACTTAA ATCATCAAAA TTTGCCAACA       900
AATATTTGAA CGTCTCTAAA TCATTATGTT TGAGTTCCGT TTTGCTATTC       950
CATAATTCCA AACCATTTGG TAGAAAGCCC AAGCTGTGAT TTTGATCTCC      1000
CCATATAGCT GAATTTAAAT CAGTGAGTTG ATTAATTTTT TCAACACAGA      1050
AATGTAATTT TGGAATGAGG AATCGAAGTT GTTCTTCTAC TTGCTGTACT      1100
```

```
TTTCTTTTGT TTTCAATAAA ATTTCTACAC CATACTGTTA TCAAACCGCC      1150
AATTATTGTG CACAATCCTC CAATGATTGT AGATAAAATT GACAATATAT      1200
TACACACCTT TCTTAGAGGT TTATTAACAT CTATTTTTGA ATTTAAAATT      1250
ATTACTTTGG TAGCGTTATA ACCTATTTAA CAGATTAGAG AAAAATTGAA      1300
TGATCGATTG AAGAATTTCC AAAATACCGT CCCATATGCG TTGAAGGAGA      1350
TTTCTATTTT CTTCTGTATT CAAATCTTTG GCTTTATCCT TTGCTTTATT      1400
CAATAAATCA TCTGAGTTTT TTTCAATATT TTTTAATACA TCTTTGGCAT      1450
TTTGTTTAAA TACTTTAGGA TCGGAAGTTA GGGCATTAGA GTTTGCCACA      1500
TTAATCATAT TATTATTAAT CATTTGAATT TGATTATCTG ATAATATCTC      1550
TGATAACCTA CGCTCATCGA GGACTTTATT AACAGTGTCT TCAACTTGTT      1600
GTTGTGTGAT TTGTTTATCT TGATTTTGTT TAATATCTGC AAGTTGTTCT      1650
TTAATATCTG CTATAGAAGC ATTTAAAGCT TCATCTGAAT ACCCAT         1696
```

2) INFORMATION FOR SEQ ID NO: 51

(i) (A) LENGTH: 2122 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

```
GGAAACTAAA AGAGAAATAT TGGAAGCAAG CCATAGCAGA ATATGAAAAA        50
CGTTTAGGCC CATACACCAA GATAGACATC ATAGAAGTTC CAGACGAAAA       100
AGCACCAGAA AATATGAGCG ACAAAGAAAT TGAGCAAGTA AAAGAAAAAG       150
AAGGCCAACG AATACTAGCC AAAATCAAAC CACAATCAAC AGTCATTACA       200
TTAGAAATAC AAGGAAAGAT GCTATCTTCC GAAGGATTGG CCCAAGAATT       250
GAACCAACGC ATGACCCAAG GGCAAAGCGA CTTTGTATTC GTCATTGGCG       300
GATCAAACGG CCTGCACAAG GACGTCTTAC AACGCAGTAA CTACGCACTA       350
TCATTCAGCA AAATGACATT CCCACATCAA ATGATGCGGG TTGTGTTAAT       400
TGAACAAGTG TACAGAGCAT TTAAGATTAT GCGTGGAGAA GCGTACCACA       450
AATGATGCGG TTTTTTATCC AGTTTTTTGT TTAATGAACA AGGTAAATTA       500
CGAGATAATA TTTGAAGAAA ACAATAAAGT AGAGATGGAT TTCCATATCC       550
TCTTTAGTAG CGGTTTTTAT CTGTAAGGTT TATTAATAAT TAAATAAATA       600
GGCGGGATAG TTATATATAG CTTATTAATG AAAGAATATG ATTATTAATT       650
TAGTATTATA TTTTAATATT AAAAAGAAGA TATGAAATAA TTATTCATAC       700
CTTCCACCTT ACAATAATTA GTTTTCAATC GAATATTAAG ATTATTAGTA       750
GTCTTAAAAG TTAAGACTTC CTTATATTAA TGACCTAATT TATTATTTGC       800
CTCATGAATT ATCTTTTTAT TTCTTTGATA TGTCCCAAAC CACATCGTGA       850
TATACACTAC AATAAATATT ATGATGAAAC TAATAATATT CTCAAAGTTC       900
AGATGGAACC AACCTGCTAG AATAGCGAGT GGGAAGAATA GGATTATCAT       950
CAATATAAAG TGAACTACAG TCTGTTTTGT TATACTCCAA TCGGTATCTG      1000
TAAATATCAA ATTACCATAA GTAAACAAAA TTCCAATCAA TGCCCATAGT      1050
GCTACACATA TTAGCATAAT AACCGCTTCA TTAAAGTTTT CATAATAAAT      1100
TTTACCCATA AAAGAATCTG GATATAGTGG TACATATTTA TCCCTTGAAA      1150
AAAATAAGTG AAGTAATGAC AGAAATCATA AGACCAGTGA ACGCACCTTT      1200
TTGAACAGCG TGGAATAATT TTTTCATAGT GAGATGGACC ATTCCATTTG      1250
TTTCTAACTT CAAGTGATCA ATGTAATTTA GATTGATAAT TTCTGATTTT      1300
GAAATACGCA CGAATATTGA ACCGACAAGC TCTTCAATTT GGTAAAGTCG      1350
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CTGATAAAGT TTTAAAGCTT TATTATTCAT TGTTATCGCA TACCTGTTTA      1400
TCTTCTACTA TGAACTGTGC AATTTGTTCT AGATCAATTG GGTAAACATG      1450
ATGGTTCTGT TGCAAAGTAA AAAAATATAG CTAACCACTA ATTTATCATG      1500
TCAGTGTTCG CTTAACTTGC TAGCATGATG CTAATTTCGT GGCATGGCGA      1550
AAATCCGTAG ATCTGATGAG ACCTGCGGTT CTTTTTATAT AGAGCGTAAA      1600
TACATTCAAT ACCTTTTAAA GTATTCTTTG CTGTATTGAT ACTTTGATAC      1650
CTTGTCTTTC TTACTTTAAT ATGACGGTGA TCTTGCTCAA TGAGGTTATT      1700
CAGATATTTC GATGTACAAT GACAGTCAGG TTTAAGTTTA AAAGCTTTAA      1750
TTACTTTAGC CATTGCTACC TTCGTTGAAG GTGCCTGATC TGTAATTACC      1800
TTTTGAGGTT TACCAAATTG TTTAATGAGA CGTTTGATAA ACGCATATGC      1850
TGAATGATTA TCTCGTTGCT TACGCAACCA AATATCTAAT GTATGTCCCT      1900
CTGCATCAAT GGCACGATAT AAATAGCTCC ATTTTCCTTT TATTTTGATG      1950
TACGTCTCAT CAATACGCCA TTTGTAATAA GCTTTTTTAT GCTTTTTCTT      2000
CCAAATTTGA TACAAAATTG GGGCATATTC TTGAACCCAA CGGTAGACCG      2050
TTGAATGATG AACGTTTACA CCACGTTCCC TTAATATTTC AGATATATCA      2100
CGATAACTCA ATGTATATCT TA                                    2122
```

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

GATAGACTAA TTATCTTCAT C **21**

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

CAGACTGTGG ACAAACTGAT T **21**

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

TGAGATCATC TACATCTTTA **20**

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

GGATCAAAAG CTACTAAATC **20**

2) INFORMATION FOR SEQ ID NO: 56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

ATGCTCTTTG TTTTGCAGCA **20**

2) INFORMATION FOR SEQ ID NO: 57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

ATGAAAGACT GCGGAGGCTA ACT 23

2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

ATATTCTAGA TCATCAATAG TTG 23

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

AAGAATTGAA CCAACGCATG A 21

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

GTTCAAGCCC AGAAGCGATG T **21**

2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

TCGGGCATAA ATGTCAGGAA AAT **23**

2) INFORMATION FOR SEQ ID NO: 62

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

AAACGACATG AAAATCACCA T **21**

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

TTATTAGGTA AACCAGCAGT AAGTGAACAA CCA **33**

2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

GGATCAAACG GCCTGCACA **19**

2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

CACAGAAATG TAATTTTGGA ATGAGG **26**

2) INFORMATION FOR SEQ ID NO: 66

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

GTCAAAAATC ATGAACCTCA TTACTTATG **29**

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

ATTTCATATA TGTAATTCCT CCACATCTC **29**

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

TCTACGGATT TTCGCCATGC **20**

2) INFORMATION FOR SEQ ID NO: 69

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

AACAGGTGAA TTATTAGCAC TTGTAAG **27**

2) INFORMATION FOR SEQ ID NO: 70

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

ATCAAATGAT GCGGGTTGTG T **21**

2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

TCATTGGCGG ATCAAACGG **19**

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

ACAACGCAGT AACTACGCAC TA **22**

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

TAACTACGCA CTATCATTCA GC **22**

2) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

ACATCAAATG ATGCGGGTTG TG **22**

2) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

TCAAATGATG CGGGTTGTGT TA **22**

2) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

CAAATGATGC GGGTTGTGTT AATT **24**

2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

CTACTATGAA CTGTGCAATT TGTTCT **26**

2) INFORMATION FOR SEQ ID NO: 78

(i) (A) LENGTH: 2007 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC 8325
(C) ACCESSION NUMBER: Extracted from X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

```
ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG        50
GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA       100
TTGATGCAAT TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT       150
TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT       200
AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA       250
AAATAAAAAA AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA       300
ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT       350
TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC GTCATTATTC       400
CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA       450
CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC       500
ACATATGAGA TTAGGCATCG TTCCAAAGAA TGTATCTAAA AAAGATTATA       550
AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAACAACAAA       600
TGGATCAAAA TTGGGTACAA GATGATACCT TCGTTCCACT TTAAAACCGT       650
TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA       700
CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA       750
CATCTATTAG GTTATGTTGG TCCCATTAAC TCTGAAGAAT TAAAACAAAA       800
AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG       850
AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA       900
ATCGTTGACG ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA       950
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GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA      1000
AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG TACTGCTATC      1050
CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA      1100
CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA      1150
CCGAAGATAA AAAAGAACCT CTGCTCAACA AGTTCCAGAT TACAACTTCA      1200
CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA      1250
AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA      1300
AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT      1350
GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT      1400
TGCTAGAGTA GCACTCGAAT TAGGCAGTAA GAAATTTGAA AAAGGCATGA      1450
AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT      1500
GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC      1550
AGGTTACGGA CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA      1600
TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA      1650
AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT CCAAAGAAAA      1700
TATCAATCTA TTAAATGATG GTATGCAACA AGTCGTAAAT AAAACACATA      1750
AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT      1800
GCAGAACTCA AAATGAAACA AGGAGAAAGT GGCAGACAAA TTGGGTGGTT      1850
TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA      1900
AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT      1950
AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA      2000
TGAATAA                                                    2007
```

2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

CAAATATTAT CTCGTAATTT ACCTTGTTC **29**

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

CTCTGCTTTA TATTATAAAA TTACGGCTG 29

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

ATTGCTGTTA ATATTTTTTG AGTTGAA 27

2) INFORMATION FOR SEQ ID NO: 82

(i) (A) LENGTH: 2007 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC 10442
(C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

```
ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG      50
GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA     100
TTGATGCAAT TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT     150
TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT     200
AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA     250
AAATAAAAAA AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA     300
ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT     350
TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC GTCATTATTC     400
CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA     450
CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC     500
AGCATATGAG ATAGGCATCG TTCCAAAGAA TGTATCTAAA AAAGATTATA     550
AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA     600
ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT     650
TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA     700
CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA     750
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```
CATCTATTAG GTTATGTTGG TCCCATTAAC TCTGAAGAAT TAAAACAAAA      800
AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG      850
AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA      900
ATCGTTGACG ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA      950
GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA     1000
AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG TACTGCTATC     1050
CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA     1100
CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA     1150
CCGAAGATAA AAAAGAACCT CTGCTCAACA AGTTCCAGAT TACAACTTCA     1200
CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA     1250
AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA     1300
AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT     1350
GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT     1400
TGCTAGAGTA GCACTCGAAT TAGGCAGTAA GAAATTTGAA AAAGGCATGA     1450
AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT     1500
GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC     1550
AGGTTACGGA CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA     1600
TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA     1650
AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT CCAAAGAAAA     1700
TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA     1750
AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT     1800
GCAGAACTCA AAATGAAACA AGGAGAAACT GGCAGACAAA TTGGGTGGTT     1850
TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA     1900
AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT     1950
AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA     2000
TGAATAA                                                   2007
```

2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

CCCACCCCAC ATCAAATGAT GCGGGTTGTG GGTGGG **36**

2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

CCCGCGCGTA GTTACTGCGT TGTAAGACGT CCGCGGG 37

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

GTTTTTATCA CCATATTGAA TTTATAC 27

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

ATTTACTTGA AAGACTGCGG AGGAG 25

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

TGTTTGAGCT TCCACAGCTA TTTC **24**

2) INFORMATION FOR SEQ ID NO: 88

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

CCCTATAATT CCAATTATTG CACTAAC **27**

2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

ATGAGGAGAT AATAATTTGG AGGGT **25**

2) INFORMATION FOR SEQ ID NO: 90

(i) (A) LENGTH: 2007 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: N315
(C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

```
ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG      50
GTTTGGTATA TATTTTTATG CTTCCAAAGA TAAAGAAATT AATAATACTA     100
TTGATGCAAT TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT     150
TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT     200
AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA     250
AAATAAAAAA AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA     300
ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT     350
TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC GTCATTATTC     400
CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA     450
CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC     500
AGCATATGAG ATAGGCATCG TTCCAAAGAA TGTATCTAAA AAAGATTATA     550
AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA     600
ATGGATCAAA ATTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT     650
TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA     700
CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGGAAA AGCGACTTCA     750
CATCTATTAG GTTATGTTGG TCCCATTAAC TCTGAAGAAT TAAAACAAAA     800
AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG     850
AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA     900
ATCGTTGACG ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA     950
GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA    1000
AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG TACTGCTATC    1050
CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA    1100
CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA    1150
CCGAAGATAA AAAAGAACCT CTGCTCAACA AGTTCCAGAT TACAACTTCA    1200
CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA    1250
AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA    1300
AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT    1350
GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT    1400
TGCTAGAGTA GCACTCGAAT TAGGCAGTAA GAAATTTGAA AAAGGCATGA    1450
AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT    1500
GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC    1550
AGGTTACGGA CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA    1600
TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA    1650
AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT CCAAAGAAAA    1700
TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA    1750
AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT    1800
GCAGAACTCA AAATGAAACA AGGAGAAACT GGCAGACAAA TTGGGTGGTT    1850
TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA    1900
AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT    1950
AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA    2000
TGAATAA                                                  2007
```

2) INFORMATION FOR SEQ ID NO: 91

(i) (A) LENGTH: 2007 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/2082
(C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

```
ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG      50
GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA     100
TTGATGCAAT TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT     150
TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT     200
AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA     250
AAATAAAAAA AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA     300
ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT     350
TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC GTCATTATTC     400
CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA     450
CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC     500
AGCATATGAG ATAGGCATCG TTCCAAAGAA TGTATCTAAA AAAGATTATA     550
AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAAACAACAA     600
ATGGATCAAA AGTGGGTACA AGATGATACC TTCGTTCCAC TTAAAACCGT     650
TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA     700
CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA     750
CATCTATTAG GTTATGTTGG TCCCATTAAC TCTGAAGAAT TAAAACAAAA     800
AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG     850
AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA     900
ATCGTTGACG ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA     950
GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA    1000
AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG TACTGCTATC    1050
CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA    1100
CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA    1150
CCGAAGATAA AAAAGAACCT CTGCTCAACA AGTTCCAGAT TACAACTTCA    1200
CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA    1250
AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA    1300
AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT    1350
GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT    1400
TGCTAGAGTA GCACTCGAAT TAGGCAGTAA GAAATTTGAA AAAGGCATGA    1450
AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT    1500
GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC    1550
AGGTTACGGA CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA    1600
TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA    1650
AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT CCAAAGAAAA    1700
TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT AAAACACATA    1750
AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT    1800
GCAGAACTCA AAATGAAACA AGGAGAAACT GGCAGACAAA TTGGGTGGTT    1850
TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA    1900
AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT    1950
AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA    2000
TGAATAA                                                  2007
```

2) INFORMATION FOR SEQ ID NO: 92

(i) (A) LENGTH: 675 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC 10442
(C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

```
ATGAACTATT TCAGATATAA ACAATTTAAC AAGGATGTTA TCACTGTAGC      50
CGTTGGCTAC TATCTAAGAT ATACATTGAG TTATCGTGAT ATATCTGAAA     100
TATTAAGGGA ACGTGGTGTA AACGTTCATC ATTCAACGGT CTACCGTTGG     150
GTTCAAGAAT ATGCCCCAAT TTTGTATCAA ATTTGGAAGA AAAAGCATAA     200
AAAAGCTTAT TACAAATGGC GTATTGATGA GACGTACATC AAAATAAAAG     250
GAAAATGGAG CTATTTATAT CGTGCCATTG ATGCAGAGGG ACATACATTA     300
GATATTTGGT TGCGTAAGCA ACGAGATAAT CATTCAGCAT ATGCGTTTAT     350
CAAACGTCTC ATTAAACAAT TTGGTAAACC TCAAAAGGTA ATTACAGATC     400
AGGCACCTTC AACGAAGGTA GCAATGGCTA AAGTAATTAA AGCTTTTAAA     450
CTTAAACCTG ACTGTCATTG TACATCGAAA TATCTGAATA ACCTCATTGA     500
GCAAGATCAC CGTCATATTA AAGTAAGAAA GACAAGGTAT CAAAGTATCA     550
ATACAGCAAA GAATACTTTA AAAGGTATTG AATGTATTTA CGCTCTATAT     600
AAAAAGAACC GCAGGTCTCT TCAGATCTAC GGATTTTCGC CATGCCACGA     650
AATTAGCATC ATGCTAGCAA GTTAA                                675
```

2) INFORMATION FOR SEQ ID NO: 93

(i) (A) LENGTH: 675 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: N315
(C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

```
ATGAACTATT TCAGATATAA ACAATTTAAC AAGGATGTTA TCACTGTAGC      50
```

```
CGTTGGCTAC TATCTAAGAT ATACATTGAG TTATCGTGAT ATATCTGAAA      100
TATTAAGGGA ACGTGGTGTA AACGTTCATC ATTCAACGGT CTACCGTTGG      150
GTTCAAGAAT ATGCCCCAAT TTTGTATCAA ATTTGGAAGA AAAAGCATAA      200
AAAAGCTTAT TACAAATGGC GTATTGATGA GACGTACATC AAAATAAAAG      250
GAAAATGGAG CTATTTATAT CGTGCCATTG ATGCAGAGGG ACATACATTA      300
GATATTTGGT TGCGTAAGCA ACGAGATAAT CATTCAGCAT ATGCGTTTAT      350
CAAACGTCTC ATTAAACAAT TTGGTAAACC TCAAAAGGTA ATTACAGATC      400
AGGCACCTTC AACGAAGGTA GCAATGGCTA AAGTAATTAA AGCTTTTAAA      450
CTTAAACCTG ACTGTCATTG TACATCGAAA TATCTGAATA ACCTCATTGA      500
GCAAGATCAC CGTCATATTA AAGTAAGAAA GACAAGGTAT CAAAGTATCA      550
ATACAGCAAA GAATACTTTA AAAGGTATTG AATGTATTTA CGCTCTATAT      600
AAAAAGAACC GCAGGTCTCT TCAGATCTAC GGATTTTCGC CATGCCACGA      650
AATTAGCATC ATGCTAGCAA GTTAA                                 675
```

2) INFORMATION FOR SEQ ID NO: 94

(i) (A) LENGTH: 675 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: HUC19
(C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

```
ATGAACTATT TCAGATATAA ACAATTTAAC AAGGATGTTA TCACTGTAGC       50
CGTTGGCTAC TATCTAAGAT ATACATTGAG TTATCGTGAT ATATCTGAAA      100
TATTAAGGGA ACGTGGTGTA AACGTTCATC ATTCAACGGT CTACCGTTGG      150
GTTCAAGAAT ATGCCCCAAT TTTGTATCAA ATTTGGAAGA AAAAGCATAA      200
AAAAGCTTAT TACAAATGGC GTATTGATGA GACGTACATC AAAATAAAAG      250
GAAAATGGAG CTATTTATAT CGTGCCATTG ATGCAGAGGG ACATACATTA      300
GATATTTGGT TGCGTAAGCA ACGAGTTAAT CATTCAGCAT ATGCGTTTAT      350
CAAACGTCTC ATTAAACAAT TTGGTAAACC TCAAAAGGTA ATTACAGATC      400
AGGCACCTTC AACGAAGGTA GCAATGGCTA AAGTAATTAA AGCTTTTAAA      450
CTTAAACCTG ACTGTCATTG TACATCGAAA TATCTGAATA ACCTCATTGA      500
GCAAGATCAC CGTCATATTA AAGTAAGAAA GACAAGGTAT CAAAGTATCA      550
ATACAGCAAA GAATACTTTA AAAGGTATTG AATGTATTCA CGCTCTATAT      600
AAAAAGAACC GCAGGTCTCT TCAGATCTAC GGATTTTCGC CATGCCACGA      650
AATTAGCATC ATGCTAGCAA GTTAA                                 675
```

2) INFORMATION FOR SEQ ID NO: 95

(i) (A) LENGTH: 675 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC 8325
(C) ACCESSION NUMBER: Extracted from X53818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

```
ATGAACTATT TCAGATATAA ACAATTTAAC AAGGATGTTA TCACTGTAGC      50
CGTTGGCTAC TATCTAAGAT ATACATTGAG TTATCGTGAT ATATCTGAAA     100
TATTAAGGGA ACGTGGTGTA AACGTTCATC ATTCAACGGT CTACCGTTGG     150
GTTCAAGAAT ATGCCCCAAT TTTGTATCAA ATTTGGAAGA AAAAGCATAA     200
AAAAGCTTAT TACAAATGGC GTATTGATGA GACGTACATC AAAATAAAAG     250
GAAAATGGAG CTATTTATAT CGTGCCATTG ATGCAGAGGG ACATACATTA     300
GATATTTGGT TGCGTAAGCA ACGAGATAAT CATTCAGCAT ATGCGTTTAT     350
CAAACGTCTC ATTAAACAAT TTGGTAAACC TCAAAAGGTA ATTACAGATC     400
AGGCACCTTC AACGAAGGTA GCAATGGCTA AAGTAATTAA AGCTTTTAAA     450
CTTAAACCTG ACTGTCATTG TACATCGAAA TATCTGAATA ACCTCATTGA     500
GCAAGATCAC CGTCATATTA AAGTAAGAAA GACAAGGTAT CAAAGTATCA     550
ATACAGCAAA GAATACTTTA AAAGGTATTG AATGTATTTA CGCTCTATAT     600
AAAAAGAACC GCAGGTCTCT TCAGATCTAC GGATTTTCGC CATGCCACGA     650
AATTAGCATC ATGCTAGCAA GTTAA                                675
```

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

GTAAAGTGTA TGATGAGCTA TATGAGAA **28**

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

GCTGAAAAAA CCGCATCATT TRTGRTA **27**

2) INFORMATION FOR SEQ ID NO: 98

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

TTTAGTTTTA TTTATGATAC GCTTCTCCA **29**

2) INFORMATION FOR SEQ ID NO: 99

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

GCTGAAAAAA CCGCATCATT TATGATA **27**

2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

CTATGTCAAA AATCATGAAC CTCATTAC **28**

2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

GGAGGCTAAC TATGTCAAAA ATC **23**

2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

CTCTATAAAC ATCGTATGAT ATTGC **25**

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

ACCAAACGAC ATGAAAATCA **20**

2) INFORMATION FOR SEQ ID NO: 104

(i) (A) LENGTH: 1256 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: 85/2082
(C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

```
TTCAGAAAAA TGATTAATGT GTTTCAATAA AATCTCTCCT TCTTTGTGAA      50
CATATTCATT TTTATACTAA TTAATATAAT TTCCAAAAAA GTTTCTGTTT     100
AAAAGTGAAA AATATTATTT ACCGTTTGAC TTAAATCTTC AATATATAGG     150
TGTTTATATG TATCATTTTG CGCCAATTTG AATAAACGGG AATCAAGTCT     200
GTTTCTGAGT TTATTTCAAC TTTCTTATAG TAAACATTGT CTTAATATGA     250
TGAACTTCAA TAAAACTTTC CCTATGCCCC ATAAAATTTT CTCAAAATCA     300
AAAATAACAT ACCTTACAAC TTTTACCGTC GATATCAATT GCTCTTTTCT     350
TAATTTAGGA TTGCTTTCAA ATTTTGTACT ATAACGTGAA ACTACTTTTC     400
CTTCTTTATA ATTAAAATTT ACTAATTCAC AATCATTTTT ACTTCCATTT     450
ACAAAAACAT CCACTGTTTC TAACACAAAA TCTAATAAAC TTCCTTTTAT     500
TAATCGTAGG CATTGTATAT TTCCTTTCAT TCTTTCTTGA TTCCATTAGT     550
TTAAATTTAA AATTTCATCC ATCAATTTCT TAATTTAATT GTAGTTCCAT     600
AATCAATATA ATTTGTACAG TTATTATATA TTCTAGATCA TCAATAGTTG     650
AAAAATGGTT TATTAAACAC TCTATAAACA TCGTATGATA TTGCAAGGTA     700
TAATCCAATA TTTCATATAT GTAATTCCTC CACATCTCAT TAAATTTTTA     750
AATTATACAC AACCTAATTT TTAGTTTTAT TTATGATACG CTTCTCCACG     800
CATAATCTTA AATGCTCTGT ACACTTGTTC AATTAACACA ACCCGCATCA     850
TTTGATGTGG GAATGTCATT TTGCTGAATG ATAGTGCGTA GTTACTGCGT     900
TGTAAGACGT CCTTGTGCAG GCCGTTTGAT CCGCCAATGA CGAATACAAA     950
GTCGCTTTGC CCTTGGGTCA TGCGTTGGTT CAATTCTTGG GCCAATCCTT    1000
CGGAAGATAG CATCTTTCCT TGTATTTCTA ATGTAATGAC TGTTGATTGT    1050
GGTTTGATTT TGGCTAGTAT TCGTTGGCCT TCTTTTTCTT TTACTTGCTC    1100
AATTTCTTTG TCGCTCATAT TTTCTGGTGC TTTTTCGTCT GGAACTTCTA    1150
TGATGTCTAT CTTGGTGTAT GGGCCTAAAC GTTTTTCATA TTCTGCTATG    1200
GCTTGCTTCC AATATTTCTC TTTTAGTTTC CCTACAGCTA AAATGGTGAT    1250
TTTCAT                                                   1256
```

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

TCATGAACCT CATTACTTAT GATAAGIT 28

2) INFORMATION FOR SEQ ID NO: 106

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

GAAAAAACCG CATCATTTAT GATATGIT 28

2) INFORMATION FOR SEQ ID NO: 107

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

CCTAATTTTT AGTTTTATTT ATGATACGIT 30

2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

CACAACCTAA TTTTTAGTTT TATTTATGAT ACGIT 35

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

TGATAAGCCA TTCATTCACC CTAA 24

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

AAGGACTCCT AATTTATGTC TAATTCC 27

2) INFORMATION FOR SEQ ID NO: 111

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

ATGGGAGTCC TTCGCTATTC TGTG 24

2) INFORMATION FOR SEQ ID NO: 112

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

CACTTTTTAT TCTTCAAAGA TTTGAGC 27

2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

ATGGAAATTC TTAATCTTTA CTTGTACC 28

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

AGCATCTTCT TTACATCGCT TACT 24

2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

CAGCAATTCW CATAAACCTC ATA 23

2) INFORMATION FOR SEQ ID NO: 116

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

ACAAACTTTG AGGGGATTTT TAGTAAA 27

2) INFORMATION FOR SEQ ID NO: 117

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

TATATTGTGG CATGATTTCT TC 22

2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

CGAATGGACT AGCACTTTCT AAA 23

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

TTGAGGATCA AAAGTTGTTG C 21

2) INFORMATION FOR SEQ ID NO: 120

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

CGATGATTTT ATAGTAGGAG A 21

2) INFORMATION FOR SEQ ID NO: 121

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

TTCAATCTCT AAATCTAAAT CAGTTTTG 28

2) INFORMATION FOR SEQ ID NO: 122

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

AGGCGAGAAA ATGGAACATA TCAA 24

2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

GGTACAAGTA AAGATTAAGA ATTTCC 26

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

AGACAACTTT ATGCAGGTCC TT 22

2) INFORMATION FOR SEQ ID NO: 125

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

TAACTGCTTG GGTAACCTTA TC 22

2) INFORMATION FOR SEQ ID NO: 126

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

TATTGCAGGT TTCGATGTTG A 21

2) INFORMATION FOR SEQ ID NO: 127

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

TGACCCATAT CGCCTAAAAT AC 22

2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

AAAGGACAAC AAGGTAGCAA AG 22

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

TCTGTGGATA AACACCTTGA TG 22

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

GTTTGATCCG CCAATGAC 18

2) INFORMATION FOR SEQ ID NO: 131

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

GGCATAAATG TCAGGAAAAT ATC 23

2) INFORMATION FOR SEQ ID NO: 132

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

GAGGACCAAA CGACATGAAA ATC 23

2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

TTCGAGGTTG ATGGGAAGCA 20

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

CGCTCGACTC AGGGTGTT 18

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

CGTTGAAGAT GCCTTTGA 18

2) INFORMATION FOR SEQ ID NO: 136

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

TTTTGCAACA GCCATTCG 18

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

GCACACATGT TGTAAGTTTG C 21

2) INFORMATION FOR SEQ ID NO: 138

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

ACGCAAACTT ACAACATGTG TG 22

2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

CGTTTGTCTG ATTTGGAGGA AG 22

2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

TTTCTTCATC ATCGGTCATA AAAT 24

2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

CTACGTGAAT CAAAAACAAT GGA 23

2) INFORMATION FOR SEQ ID NO: 142

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

TACTGCAAAG TCTCGTTCAT CC 22

2) INFORMATION FOR SEQ ID NO: 143

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

CATACCATTT TGAACGATGA CCTC 24

2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

ATGTCTGGTC AACTTTCCGA CTC 23

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

CAATCGGTAT CTGTAAATAT CAAAT 25

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

TCGCATACCT GTTTATCTTC TACT 24

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

TTGGTTCCAT CTGAACTTTG AG 22

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

AATGGCTTAT CAAAGTGAAT ATGC 24

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

TAATTTCCTT TTTTTCCATT CCTC 24

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

ACTAGAATCT CCAAATGAAT CCAGT 25

2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

TGGAGTTAAT CTACGTCTCA TCTC 24

2) INFORMATION FOR SEQ ID NO: 152

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

GTTCATACAG AAGACTCCTT TTTG 24

2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

AGTTTTGATT ATCCGAATAA ATGCT 25

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

TTTAAATTCA GCTATATGGG GAGA 24

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

TTCCGTTTTG CTATTCCATA AT 22

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

CCTCTGATAA AAAACTTGTG AAAT 24

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

ACTACTCCTG GAATTACAAA CTGG 24

2)INFORMATION FOR SEQ ID NO: 158

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

GCCAAAATTA AACCACAATC CAC 23

2)INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

CATTTTGCTG AATGATAGTG CGTA 24

2)INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

CGACCGGATT CCCACATCAA ATGATGCGGG TTGTGTTAAT TCCGGTCG 48

2)INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

CCCGCGCRTA GTTACTRCGT TGTAAGACGT CCGCGGG 37

2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

CCCCGTAGTT ACTGCGTTGT AAGACGGGG 29

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CCCGCGCATA GTTACTGCGT TGTAAGACGT CCGCGGG 37

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCCGCGCGTA GTTACTACGT TGTAAGACGT CCGCGGG 37

2) INFORMATION FOR SEQ ID NO: 165

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1282 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

ACCATTTTAG CTGTAGGGAA ACTAAAAGAG AAATATTGGA AGCAAGCCAT 50
AGCAGAATAT GAAAAACGTT TAGGCCCATA CACCAAGATA GACATCATAG 100
AAGTTCCAGA CGAAAAAGCA CCAGAAAATA TGAGCGACAA AGAAATTGAG 150
CAAGTAAAAG AAAAAGAAGG CCAACGAATA CTAGCCAAAA TCAAACCACA 200
ATCCACAGTC ATTACATTAG AAATACAAGG AAAGATGCTA TCTTCCGAAG 250
GATTGGCCCA AGAATTGAAC CAACGCATGA CCCAAGGGCA AAGCGACTTT 300
GTATTCGTCA TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG 350
CAGTAACTAT GCACTATCAT TTAGCAAAAT GACATTCCCA CATCAAATGA 400
TGCGGGTTGT GTTAATTGAA CAAGTGTATA GAGCATTTAA GATTATGCGT 450
GGAGAAGCGT ACCACAAATA AAACTAAAAA ATATGAGAAA ATTATTAAAT 500
TAGCTCAAAT CTTTGAAGAA TAAAAAGTGA ATATTAAGTT TGATAATTTA 550
GGTACAAGTA AAGATTAAGA ATTTCCATTA TTTAATACAT GGTGTGTAAA 600
TCGACTTCTT TTTGTATTAG ATGTTTGCAG TAAGCGATGT AAAGAAGATG 650
CTAATAAATA TGTGAGGAAT GATTACGATA CTAGATAAGC GGCTAATGAA 700
ATTTTTTAAA GTACATATAT AGACATATTT TTCATTTAGT AAAATTTTGA 750
ATTTCACTTT GCTAAGACTA GTGTCTAGAA ATTTATAATG ATTTATTAAC 800
ACCTATTTGA AACTTAAGTA TAATAAATGA TTCGGATTTT ATTTTTAATA 850
AAGACAAACT TGAACGTAGC AAAGTAGTTT TTATGATAAA TAATAAGTTT 900
TAATAATGTG ACGCTTTTAT ATAAGCACAT TATTATGAAC AATGTGAATT 950
GAGCATCTAC AATTACATTA ATAAATATAT AAATGATGAT TTAAATTCAC 1000
ATATATTTAT AATACACATA CTATATGAAA GTTTTGATTA TCCGAATAAA 1050
TGCTAAAATT AATAAAATAA TTAAAGGAAT CATACTTATT ATACGTATAC 1100
GTTTAGCTAC TGAACTACTG GATTCATTTG GAGATTCTAG TAGTTCTTTT 1150
TCAATCTCTA AATCTAAATC AGTTTTGTAA TAACCATTAA TTCCTAATCT 1200
TTCATCTAGC TCTGTACTTT TTTCATCATT TTTATCTTTG TTGATATGTT 1250
CCATTTTCTC GCCTCTTTTT AATCAAGTAG AA 1282

2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1108 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

```
ACCATTTTAG CTGTAGGGAA ACTAAAAGAG AAATATTGGA AGCAAGCCAT        50
AGCAGAATAT GAAAAACGTT TAGGCCCATA CACCAAGATA GACATCATAG       100
AAGTTCCAGA CGAAAAAGCA CCAGAAAATA TGAGCGACAA AGAAATTGAG       150
CAAGTAAAAG AAAAAGAAGG CCAACGAATA CTAGCCAAAA TCAAACCACA       200
ATCCACAGTC ATTACATTAG AAATACAAGG AAAGATGCTA TCTTCCGAAG       250
GATTGGCCCA AGAATTGAAC CAACGCATGA CCCAAGGGCA AAGCGACTTT       300
GTATTCGTCA TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG       350
CAGTAACTAT GCACTATCAT TTAGCAAAAT GACATTCCCA CATCAAATGA       400
TGCGGGTTGT GTTAATTGAA CAAGTGTATA GAGCATTTAA GATTATGCGT       450
GGAGAAGCGT ACCACAAATA AAACTAAAAA ATATGAGAAA ATTATTAAAT       500
TAGCTCAAAT CTTTGAAGAA TAAAAAGTGA ATATTAAGTT TGATAATTTA       550
GGTACAAGTA AAGATTAAGA ATTTCCATTA TTTAATACAT GGTGTGTAAA       600
TCGACTTCTT TTTGTATTAG ATGTTTGCAG TAAGCGATGT AAAGAAGATG       650
CTAATAAATA TGTGAGGAAT GATTACGATA CTAGATAAGC GGCTAATGAA       700
ATTTTTTAAA GTACATATAT AGACATATTT TTCATTTAGT AAAATTTTGA       750
ATTTCACTTT GCTAAGACTA GTGTCTAGAA ATTTATAATG ATTTATTAAC       800
ACCTATTTGA AACTTAAGTA TAATAAATGA TTCGGATTTT ATTTTTAATA       850
AAGACAAACT TGAACGTAGC AAAGTAGTTT TTATGATAAA TAATAAGTTT       900
TAATAATGTG ACGCTTTTAT ATAAGCACAT TATTATGAAC AATGTGAATT       950
GAGCATCTAC AATTACATTA ATAAATATAT AAATGATGAT TTAAATTCAC      1000
ATATATTTAT AATACACATA CTATATGAAA GTTTTGATTA TCCGAATAAA      1050
TGCTAAAATT AATAAAATAA TTAAAGGAAT CATACTTATT ATACGTATAC      1100
GTTTAGCT                                                   1108
```

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1530 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

```
TTAGCTGTAG GGAAACTAAA AGAGAAATAT TGGAAGCAAG CCATAGCAGA        50
ATATGAAAAA CGTTTAGGCC CATACACCAA GATAGACATC ATAGAAGTTC       100
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CAGACGAAAA AGCACCAGAA AATATGAGCG ACAAAGAAAT TGAGCAAGTA      150
AAAGAAAAAG AAGGCCAACG AATACTAGCC AAAATCAAAC CACAATCCAC      200
AGTCATTACA TTAGAAATAC AAGGAAAGAT GCTATCTTCC GAAGGATTGG      250
CCCAAGAATT GAACCAACGC ATGACCCAAG GGCAAAGCGA CTTTGTATTC      300
GTCATTGGCG GATCAAACGG CCTGCACAAG GACGTCTTAC AACGCAGTAA      350
CTATGCACTA TCATTTAGCA AAATGACATT CCCACATCAA ATGATGCGGG      400
TTGTGTTAAT TGAACAAGTG TATAGAGCAT TTAAGATTAT GCGTGGAGAA      450
GCATATCATA AATGATGCGG TTTTTTCAGC CGCTTCATAA AGGGGGGTGA      500
TCATATCGGA ACGTATGAGG TTTATGAGAA TTGCTGCTAT GTTTTTATGA      550
AGCGTATCAT AAATGATGCA GTTTTTGATA ATTTTTTCTT TATCAGAGAT      600
TTTACTAAAA ATCCCCTCAA AGTTTGTTTT TTTCAACTTC AACTTTGAAG      650
GGAATAAATA AGGAACTTAT TTATATTTAT CCTTTATCTC ATTAATATCT      700
ATTTTTTTAT TAATAATATT ATAAATATTA AATTCTTTAG AAAAGTCACT      750
ATCACTCTTA TTCTTCATAC TAAACGTTAT TAATCTAATA ATATCAGCTA      800
CTATTTCTTT AAATTCTATT GCATCTTCTT TTTTATAAGT AGCGCCTGTA      850
TGAACAATTT TATTTCTCAT ACCATAGTAA TCTTTCATAT ATTTTTTTAC      900
ACAATTTTTA ATTTCATTAG AATTATCCAA ATCTAGATTA TCAATTGTCT      950
TTAATAAATG ATCATTAACA ACATTAGCAT ACCCACATCC AAGCTTCTTT     1000
TTTATCTCTT CATCACTTAA ATTTTCATCT AATTTATAAT ATCTTTCTAA     1050
AAAATTTGTG ATAAAAACTT CTAATGCAGT CTGAATTTGT ACAATTGCTA     1100
AATTATAGTC AGATTTATAA AAAGAACGTT CACCTTTTCT CATAGCCAAA     1150
ACATAAATAT TGCTAGGATG ATTATTGAAA ATATTATAAT TTTTTTTAAT     1200
ATTTAATAAA TCACTTTTTT TGATAGATGA ATACTGATCT TCTTCTATCT     1250
TTCCAGGCAT GTCAATCATG AAAATACTCA TCTCTTTTAT ATTTCCATCT     1300
ATAGTATATA TTATATAATA TGGAATACTT AATATATCCC CTAATGATAG     1350
CTGGTATATA TTATGATACT GATATTTAAC GCTAATAATT TTAATAAGAT     1400
TATTTAGACA ATTAAATTGC TTATTAAAAA TTTTCGTTAG ACTATTACTT     1450
TTCTTTGATT CCCTAGAAGT AGAATTTGAT TTCAATTTTT TAAACTGATT     1500
GTGCTTGATT ATTGAAGTTA TTTCAACATA                           1530
```

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1256 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

```
GCTGTAGGGA AACTAAAAGA GAAATATTGG AAGCAAGCCA TAGCAGAATA       50
TGAAAAACGT TTAGGCCCAT ACACCAAGAT AGACATCATA GAAGTTCCAG      100
ACGAAAAAGC ACCAGAAAAT ATGAGCGACA AAGAAATTGA GCAAGTAAAA      150
GAAAAAGAAG GCCAACGAAT ACTAGCCAAA ATTAAACCAC AATCCACAGT      200
CATTACATTA GAAATACAAG GAAAGATGCT ATCTTCCGAA GGATTGGCCC      250
AAGAATTGAA CCAACGCATG ACCCAAGGGC AAAGCGACTT TGTATTCGTC      300
ATTGGCGGAT CAAACGGCCT GCACAAGGAC GTCTTACAAC GCAGTAACTA      350
CGCACTATCA TTCAGCAAAA TGACATTCCC ACATCAAATG ATGCGGGTTG      400
TGTTAATTGA GCAAGTGTAT AGAGCATTTA AGATTATGCG TGGAGAAGCA      450
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```
TATCATAAAT GATGCGGTTT TTTCAGCCGC TTCATAAAGG GATTTTGAAT       500
GTATCAGAAC ATATGAGGTT TATGTGAATT GCTGTTATGT TTTTAAGAAG       550
CATATCATAA GTGATGCGGT TTTTATTAAT TAGTTGCTAA AAAATGAAGT       600
ATGCAATATT AATTATTATT AAATTTTGAT ATATTTAAAG AAAGATTAAG       650
TTTAGGGTGA ATGAATGGCT TATCAAAGTG AATATGCATT AGAAAATGAA       700
GTACTTCAAC AACTTGAGGA ATTGAACTAT GAAAGAGTAA ATATACATAA       750
TATTAAATTA GAAATTAATG AATATCTCAA AGAACTAGGA GTGTTGAAAA       800
ATGAATAAGC AGACAAATAC TCCAGAACTA AGATTTCCAG AGTTTGATGA       850
GGAATGGAAA AAAAGGAAAT TAGGTGAAGT AGTAAATTAT AAAAATGGTG       900
GTTCATTTGA AAGTTTAGTG AAAAACCATG GTGTATATAA ACTCATAACT       950
CTTAAATCTG TTAATACAGA AGGAAAGTTG TGTAATTCTG GAAAATATAT      1000
CGATGATAAA TGTGTTGAAA CATTGTGTAA TGATACTTTA GTAATGATAC      1050
TGAGCGAGCA AGCACCAGGA CTAGTTGGAA TGACTGCAAT TATACCTAAT      1100
AATAATGAGT ATGTACTAAA TCAACGAGTA GCAGCACTAG TGCCTAAACA      1150
ATTTATAGAT AGTCAATTTC TATCTAAGTT AATTAATAGA AACCAGAAAT      1200
ATTTCAGTGT GAGATCTGCT GGAACAAAAG TGAAAAATAT TTCTAAAGGA      1250
CATGTA                                                     1256
```

2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

```
TTACATTAGA AATACAAGGA AAGATGCTAT CTTCCGAAGG ATTGGCCCAA        50
GAATTGAACC AACGCATGAC CCAAGGGCAA AGCGACTTTG TTTTCGTCAT       100
TGGCGGATCA AACGGCCTGC ACAAGGACGT CTTACAACGC AGTAACTACG       150
CACTATCATT CAGCAAAATG ACATTCCCAC ATCAAATGAT GCGGGTTGTG       200
TTAATTGAAC AAGTGTACAG AGCATTTAAG ATTATGCGAG GAGAAGCTTA       250
TCATAAGTAA TGAGGTTCAT GATTTTTGAC ATAGTTAGCC TCCGCAGTCT       300
TTCATTTCAA GTAAATAATA GCGAAATATT CTTTATACTG AATACTTATA       350
GTGAAGCAAA GTTCTAGCTT TGAGAAAATT CTTTCTGCAA CTAAATATAG       400
TAAATTACGG TAAAATATAA ATAAGTACAT ATTGAAGAAA ATGAGACATA       450
ATATATTTTA TAATAGGAGG GAATTTCAAA TGATAGACAA CTTTATGCAG       500
GTCCTTAAAT TAATTAAAGA GAAACGTACC AATAATGTAG TTAAAAAATC       550
TGATTGGGAT AAAGGTGATC TATATAAAAC TTTAGTCCAT GATAAGTTAC       600
CCAAGCAGTT AAAAGTGCAT ATAAAAGAAG ATAAATATTC AGTTGTAGGG       650
AAGGTTGCTA CTGGGAACTA TAGTAAAGTT CCTTGGATTT CAATATATGA       700
TGAGAATATA ACAAAAGAAA CAAAGGATGG ATATTATTTG GTATATCTTT       750
TTCATCCGGA AGGAGAAGGC ATATACTTAT CTTTGAATCA AGGATGGTCA       800
AAGATAAGTG ATATGTTTCC GCGGGATAAA AATGCTGCAA AACAAA           846
```

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1270 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

```
CATTAGAAAT ACAAGGAAAG ATGCTATCTT CCGAAGGATT GGCCCAAGAA      50
TTGAACCAAC GCATGACCCA AGGGCAAAGC GACTTTGTAT TCGTCATTGG     100
CGGATCAAAC GGCCTGCACA AGGACGTCTT ACAACGCAGT AACTATGCAC     150
TATCATTTAG CAAAATGACA TTCCCACATC AAATGATGCG GGTTGTGTTA     200
ATTGAACAAG TGTATAGAGC ATTTAAGATT ATGCGTGGAG AAGCATATCA     250
TAAATGATGC GGTTTTTTCA GCCGCTTCAT AAAGGGATTT TGAATGTATC     300
AGAACATATG AGGTTTATGT GAATTGCTGT TATGTTTTTA AGAAGCTTAT     350
CATAAGTAAT GAGGTTCATG ATTTTTGACA TAGTTAGCCT CCGCAGTCTT     400
TCATTTCAAG TAAATAATAG CGAAATATTC TTTATACTGA ATACTTATAG     450
TGAAGCAAAG TTCTAGCTTT GAGAAAATTC TTTCTGCAAC TAAATATAGT     500
AAATTACGGT AAAATATAAA TAAGTACATA TTGAAGAAAA TGAGACATAA     550
TATATTTTAT AATAGGAGGG AATTTCAAAT GATAGACAAC TTTATGCAGG     600
TCCTTAAATT AATTAAAGAG AAACGTACCA ATAATGTAGT TAAAAAATCT     650
GATTGGGATA AAGGTGATCT ATATAAAACT TTAGTCCATG ATAAGTTACC     700
CAAGCAGTTA AAAGTGCATA TAAAAGAAGA TAAATATTCA GTTGTAGGGA     750
AGGTTGCTAC TGGGAACTAT AGTAAAGTTC CTTGGATTTC AATATATGAT     800
GAGAATATAA CAAAAGAAAC AAAGGATGGA TATTATTTGG TATATCTTTT     850
TCATCCGGAA GGAGAAGGCA TATACTTATC TTTGAATCAA GGATGGTCAA     900
AGATAAGTGA TATGTTTCCG CGGGATAAAA ATGCTGCAAA ACAAAGAGCA     950
TTAACTTTAT CTTCCGAACT CAATAAATAT ATTACATCAA ATGAATTTAA    1000
TACTGGAAGA TTTTATTACG CAGAAAATAA AGATTCATCT TATGATTTAA    1050
AAAATGATTA TCCATCAGGA TATTCTCATG GATCAATAAG ATTCAAATAT    1100
TATGATTTGA ATGAAGGATT CACAGAAGAA GATATGCTAG AGGATTTAAA    1150
GAAATTTTTA GAACTATTTA ATGAATTAGC TTCAAAAGTT ACAAAAACAT    1200
CCTATGATAG CTTGGTCAAT AGCATAGACG AAATACAGGA AGACAGCGAA    1250
ATTGAAGAAA TTAGAACAGC                                     1270
```

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

```
ACCATTTTAG CTGTAGGGAA ACTAAAAGAG AAATACTGGA AGCAAGCCAT        50
AGCAGAATAT GAAAAACGTT TAGGCCCATA CACCAAGATA GACATCATAG       100
AAGTTCCAGA CGAAAAAGCA CCAGAAAATA TGAACTACAA AGAAATTGAG       150
CAAGTAAAAG AAAAAGAAGG CCAACGAATA CTAGCCAAAA TCAAACCACA       200
ATCAACAGTC ATTACATTAG AAATACAAGG AAAGATGCTA TCTTCCGAAG       250
GATTGGCCCA AGAATTGAAC CAACGCATGA CCCAAGGGCA AAGCGACTTT       300
GTATTCGTCA TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG       350
CAGTAACTAC GCACTATCAT TCAGCAAAAT GACATTCCCA CATCAAATGA       400
TGCGGGTTGT GTTAATTGAA CAAGTGTACA GAGCATTTAA GATTATGCGA       450
GGAGAAGCGT ATCATAAGTG ATGGTAAAAA ATATGAGTAA GTAGATGAAG       500
AGTGAAAATC AGATTAATTA ATAATAATGT ATCAAATTTA AATAAAGGGG       550
TTTTTAAGTA TGAATTTAAG AGGTCATGAA AATAGACTTA AATTTCATGC       600
GAAATATGAT GTGACACCTA TATCACATTT AAAATTATTA GAAGGTCAAA       650
AGAAAGACGG TGAAGGCGGC ATACTGACAG ATAGCTATTA CTGTTTTTCA       700
TACAGCTTAA AAGGTAATTC TAAAAAAGTT TTAGGTACGT TTAATTGTGG       750
TTATCATATT GCTGAAGATT TACTAAAATT ATCAAATCAA GATAAATTAC       800
CTTTATTTAA CCCGTTTAAA GTAATTAATG AAGGTAATCA ATTGCAGGGC       850
GTAACGAATA AAGGTAATTT AAATATTAAT AGGCAAAGAA AACAGTATAA       900
TGAAGTGGCT TTACAGCTTT CAAATGCTAT TAATTTAATC ATAATTTGTT       950
ATGAGGATAA TATTAAAGAA CCACTTTCAA CGATAAAATA C               991
```

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 748 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

```
ATCGTTTAAC GTGTCACATG ATGCGATAGA TCCGCAATTT TATATTTTCC        50
ATAATAACTA TAAGAAGTTT ACGATTTTAA CAGATACGGG TTACGTGTCT       100
GATCGTATGA AAGGTATGAT ACGTGGCAGC GATGCATTTA TTTTTGAGAG       150
TAATCATGAC GTCGATATGT TGAGAATGTG TCGTTATCCA TGGAAGACGA       200
AACAACGCAT TTTAGGCGAT ATGGGTCATG TATCTAATGA GGATGCGGGT       250
CATGCGATGA CAGACGTGAT TACAGGTAAC ACGAAACGTA TTTACTTATC       300
GCATTTATCA CAAGATAATA ATATGAAAGA TTTGGCGCGT ATGAGTGTTG       350
GCCAAGTATT GAACGAACAC GATATTGATA CGGAAAAAGA AGTATTGCTA       400
TGTGATACGG ATAAAGCTAT TCCAACACCA ATATATACAA TATAAATGAG       450
AGTCATCCGA TAAAGTTCCG CACTGCTGTG AAACGACTTT ATCGGGTGCT       500
TTTTTATGTT GTTGGTGGGA AATGGCTGTT GTTGAGTTGA ATCGGATTGA       550
TTGAAATGTG TAAAATAATT CGATATTAAA TGTAATTTAT AAATAATTTA       600
```

```
CATAAAATCA AACATTTTAA TATAAGGATT ATGATAATAT ATTGGTGTAT      650
GACAGTTAAT GGAGGGAACG AAATGAAAGC TTTATTACTT AAAACAAGTG      700
TATGGCTCGT TTTGCTTTTT AGTGTGATGG GATTATGGCA TGTCTCGA        748
```

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

```
AAATACAAGG AAAGATGCTA TCTTCCGAAG GATTGGCCCA AGAATTGAAC       50
CAACGCATGA CCCAAGGGCA AAGCGACTTT GTATTCGTCA TTGGCGGATC      100
AAACGGCCTG CACAAGGACG TCTTACAACG TAGTAACTAC GCACTATCAT      150
TCAGCAAAAT GACATTCCCA CATCAAATGA TGCGGGTTGT GTTAATTGAG      200
CAAGTGTATA GAGCATTTAA GATTATGCGT GGAGAAGCAT ATCATAAATG      250
ATGCGGTTTT TTCAGCCGCT TCATAAAGGG ATTTTGAATG TATCAGAACA      300
TATGAGGTTT ATGTGAATTG CTGTTATGTT TTTAAGAAGC TTATCATAAG      350
TAATGAGGTT CATGATTTTT GACATAGTTA GCCTCCGCAG TCTTTCATTT      400
CAAGTAAATA ATAGCGAAAT ATTCTTTATA CTGAATACTT ATAGTGAAGC      450
AAAGTTCTAG CTTTGAGAAA ATTCTTTCTG CAACTAAATA TAGTAAATTA      500
CGGTAAAATA TAAATAAGTA CATATTGAAG AAAATGAGAC ATAATATATT      550
TTATAATAGG AGGGAATTTC AAATGATAGA CAACTTTATG CAGGTCCTTA      600
AATTAATTAA AGAGAAACGT ACCAATAATG TAGTTAAAAA ATCTGATTGG      650
GATAAAGGTG ATCTATATAA AACTTTAGTC CATGATAAGT TACCCAAGCA      700
GTTAAAAGTG CATATAAAAG AAGATAAATA TTCAGTTGTA GGGAAGGTTG      750
CTACTGGGAA CTATAGTAAA GTTCCTTGGA TTTCAATATA TGATGAGAAT      800
ATAACAAAAG AAACAAAGGA TGGATATTAT TTGGTATATC TTTTTCATCC      850
GGAAGGAGAA GGCATATACT TATCTTTGAA TCAAGGATGG TCAAAGATAA      900
GTGATATGTT TCCGCGG                                         917
```

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1132 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

```
GCTGTAGGGA AACTAAAAGA GAAATATTGG AAGCAAGCCA TAGCAGAATA      50
TGAAAAACGT TTAGGCCCAT ACACCAAGAT AGACATCATA GAAGTTCCAG     100
ACGAAAAAGC ACCAGAAAAT ATGAGCGACA AAGAAATTGA GCAAGTAAAA     150
GAAAAAGAAG GCCAACGAAT ACTAGCCAAA ATCAAACCAC AATCAACAGT     200
CATTACATTA GAAATACAAG GAAAGATGCT ATCTTCCGAA GGATTGGCCC     250
AAGAATTGAA CCAACGCATG ACCCAAGGGC AAAGCGACTT TGTATTCGTC     300
ATTGGCGGAT CAAACGGCCT GCACAAGGAC GTCTTACAAC GTAGTAACTA     350
CGCACTATCA TTCAGCAAAA TGACATTCCC ACATCAAATG ATGCGGGTTG     400
TGTTAATTGA GCAAGTGTAT AGAGCATTTA AGATTATGCG TGGAGAAGCA     450
TATCATAAAT GATGCGGTTT TTTCAGCCGC TTCATAAAGG GATTTTGAAT     500
GTATCAGAAC ATATGAGGTT TATGTGAATT GCTGTTATGT TTTTAAGAAG     550
CTTATCATAA GTAATGAGGT TCATGATTTT TGACATAGTT AGCCTCCGCA     600
GTCTTTCATT TCAAGTAAAT AATAGCGAAA TATTCTTTAT ACTGAATACT     650
TATAGTGAAG CAAAGTTCTA GCTTTGAGAA AATTCTTTCT GCAACTAAAT     700
ATAGTAAATT ACGGTAAAAT ATAAATAAGT ACATATTGAA GAAAATGAGA     750
CATAATATAT TTTATAATAG GAGGGAATTT CAAATGATAG ACAACTTTAT     800
GCAGGTCCTT AAATTAATTA AAGAGAAACG TACCAATAAT GTAGTTAAAA     850
AATCTGATTG GGATAAAGGT GATCTATATA AAACTTTAGT CCATGATAAG     900
TTACCCAAGC AGTTAAAAGT GCATATAAAA GAAGATAAAT ATTCAGTTGT     950
AGGGAAGGTT GCTACTGGGA ACTATAGTAA AGTTCCTTGG ATTTCAATAT    1000
ATGATGAGAA TATAACAAAA GAAACAAAGG ATGGATATTA TTTGGTATAT    1050
CTTTTTCATC CGGAAGGAGA AGGCATATAC TTATCTTTGA ATCAAGGATG    1100
GTCAAAGATA AGTGATATGT TTCCGCGGGA TA                       1132
```

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1133 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

```
AGCTGTAGGG AAACTAAAAG AGAAATATTG GAAGCAAGCC ATAGCAGAAT      50
ATGAAAAACG TTTAGGCCCA TACACCAAGA TAGACATCAT AGAAGTTCCA     100
GACGAAAAAG CACCAGAAAA TATGAGCGAC AAAGAAATTG AGCAAGTAAA     150
AGAAAAAGAA GGCCAACGAA TACTAGCCAA AATCAAACCA CAATCAACAG     200
TCATTACATT AGAAATACAA GGAAAGATGC TATCTTCCGA AGGATTGGCC     250
CAAGAATTGA ACCAACGCAT GACCCAAGGG CAAAGCGACT TTGTATTCGT     300
CATTGGCGGA TCAAACGGCC TGCACAAGGA CGTCTTACAA CGTAGTAACT     350
ACGCACTATC ATTCAGCAAA ATGACATTCC CACATCAAAT GATGCGGGTT     400
GTGTTAATTG AGCAAGTGTA TAGAGCATTT AAGATTATGC GTGGAGAAGC     450
```

```
ATATCATAAA TGATGCGGTT TTTTCAGCCG CTTCATAAAG GGATTTTGAA      500
TGTATCAGAA CATATGAGGT TTATGTGAAT TGCTGTTATG TTTTTAAGAA      550
GCTTATCATA AGTAATGAGG TTCATGATTT TTGACATAGT TAGCCTCCGC      600
AGTCTTTCAT TTCAAGTAAA TAATAGCGAA ATATTCTTTA TACTGAATAC      650
TTATAGTGAA GCAAAGTTCT AGCTTTGAGA AAATTCTTTC TGCAACTAAA      700
TATAGTAAAT TACGGTAAAA TATAAATAAG TACATATTGA AGAAAATGAG      750
ACATAATATA TTTTATAATA GGAGGGAATT TCAAATGATA GACAACTTTA      800
TGCAGGTCCT TAAATTAATT AAAGAGAAAC GTACCAATAA TGTAGTTAAA      850
AAATCTGATT GGGATAAAGG TGATCTATAT AAAACTTTAG TCCATGATAA      900
GTTACCCAAG CAGTTAAAAG TGCATATAAA AGAAGATAAA TATTCAGTTG      950
TAGGGAAGGT TGCTACTGGG AACTATAGTA AAGTTCCTTG GATTTCAATA     1000
TATGATGAGA ATATAACAAA AGAAACAAAG GATGGATATT ATTTGGTATA     1050
TCTTTTTCAT CCGGAAGGAG AAGGCATATA CTTATCTTTG AATCAAGGAT     1100
GGTCAAAGAT AAGTGATATG TTTCCGCGGG ATA                       1133
```

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1087 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

```
ACTAAAAGAG AAATATTGGA AGCAAGCCAT AGCAGAATAT GAAAAACGTT       50
TAGGCCCATA CACCAAGATA GACATCATAG AAGTTCCAGA CGAAAAAGCA      100
CCAGAAAATA TGAGCGACAA AGAAATTGAG CAAGTAAAAG AAAAAGAAGG      150
CCAACGAATA CTAGCCAAAA TCAAACCACA ATCAACAGTC ATTACATTAG      200
AAATACAAGG AAAGATGCTA TCTTCCGAAG GATTGGCACA AGAATTGAAC      250
CAACGCATGA CCCAAGGGCA AAGCGACTTT GTATTCGTCA TTGGCGGATC      300
AAACGGCCTG CACAAGGACG TCTTACAACG TAGTAACTAC GCACTATCAT      350
TCAGCAAAAT GACATTCCCA CATCAAATGA TGCGGGTTGT GTTAATTGAG      400
CAAGTGTATA GAGCGTTTAA GATTATGCGT GGAGAAGCAT ATCATAAATG      450
ATGCGGTTTT TTCAGCCGCT TCATAAAGGG ATTTTGAATG TATCAGAACA      500
TATGAGGTTT ATGTGAATTG CTGTTATGTT TTTAAGAAGC TTATCATAAG      550
TAATGAGGTT CATGATTTTT GACATAGTTA GCCTCCGCAG TCTTTCATTT      600
CAAGTAAATA ATAGCGAAAT ATTCTTTATA CTGAATACTT ATAGTGAAGC      650
AAAGTTCTAG CTTTGAGAAA ATTCTTTCTG CAACTAAATA TAGTAAATTA      700
CGGTAAAATA TAAATAAGTA CATATTGAAG AAAATGAGAC ATAATATATT      750
TTATAATAGG AGGGAATTTC AAATGATAGA CAACTTTATG CAGGTCCTTA      800
AATTAATTAA AGAGAAACGT ACCAATAATG TAGTTAAAAA ATCTGATTGG      850
GATAAAGGTG ATCTATATAA AACTTTAGTC CATGATAAGT TACCCAAGCA      900
GTTAAAAGTG CATATAAAAG AAGATAAATA TTCAGTTGTA GGGAAGGTTG      950
CTACTGGGAA CTATAGTAAA GTTCCTTGGA TTTCAATATA TGATGAGAAT     1000
ATAACAAAAG AAACAAAGGA TGGATATTAT TTGGTATATC TTTTTCATCC     1050
GGAAGGAGAA GGCATATACT TATCTTTGAA TCAAGGA                   1087
```

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

CAAGGAAAGA TGCTATCTTC CGAAGGATTG GCCCAAGAAT TGAACCAACG 50
CATGACCCAA GGGCAAAGCG ACTTTGTATT CGTCATTGGC GGATCAAACG 100
GCCTGCACAA GGACGTCTTA CAACGTAGTA ACTACGCACT ATCATTCAGC 150
AAAATGACAT TCCCACATCA AATGATGCGG GTTGTGTTAA TTGAGCAAGT 200
GTATAGAGCA TTTAAGATTA TGCGTGGAGA AGCATATCAT AAATGATGCG 250
GTTTTTTCAG CCGCTTCATA AAGGGATTTT GAATGTATCA GAACATATGA 300
GGTTTATGTG AATTGCTGTT ATGTTTTTAA GAAGCTTATC ATAAGTAATG 350
AGGTTCATGA TTTTTGACAT AGTTAGCCTC CGCAGTCTTT CATTTCAAGT 400
AAATAATAGC GAAATATTCT TTATACTGAA TACTTATAGT GAAGCAAAGT 450
TCTAGCTTTG AGAAAATTCT TTCTGCAACT AAATATAGTA AATTACGGTA 500
AAATATAAAT AAGTACATAT TGAAGAAAAT GAGACATAAT ATATTTTATA 550
ATAGGAGGGA ATTTCAAATG ATAGACAACT TTATGCAGGT CCTTAAATTA 600
ATTAAAGAGA AACGTACCAA TAATGTAGTT AAAAAATCTG ATTGGGATAA 650
AGGTGATCTA TATAAAACTT TAGTCCATGA TAAGTTACCC AAGCAGTTAA 700
AAGTGCATAT AAAAGAAGAT AAATATTCAG TTGTAGGGAA GGTTGCTACT 750
GGGAACTATA GTAAAGTTCC TTGGATTTCA ATATATGATG AGAATATAAC 800
AAAAGAAACA AAGGATGGAT ATTATTTGGT ATATCTTTTT CATCCGGAAG 850
GAGAAGGCAT ATACTTATCT TTGAATCAAG GATGGTCAAA GATAAGTGAT 900
ATG 903

2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1114 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

```
GGAAACTAAA AGAGAAATAT TGGAAGCAAG CCATAGCAGA ATATGAAAAA      50
CGTTTAGGCC CATACACCAA GATAGACATC ATAGAAGTTC CAGACGAAAA     100
AGCACCAGAA AATATGAGCG ACAAAGAAAT TGAGCAAGTA AAAGAAAAAG     150
AAGGCCAACG AATACTAGCC AAAATCAAAC CACAATCAAC AGTCATTACA     200
TTAGAAATAC AAGGAAAGAT GCTATCTTCC GAAGGATTGG CCCAAGAATT     250
GAACCAACGC ATGACCCAAG GGCAAAGCGA CTTTGTATTC GTCATTGGCG     300
GATCAAACGG CCTGCACAAG GACGTCTTAC AACGTAGTAA CTACGCACTA     350
TCATTCAGCA AAATGACATT CCCACATCAA ATGATGCGGG TTGTGTTAAT     400
TGAGCAAGTG TATAGAGCAT TTAAGATTAT GCGTGGAGAA GCATATCATA     450
AATGATGCGG TTTTTTCAGC CGCTTCATAA AGGGATTTTG AATGTATCAG     500
AACATATGAG GTTTATGTGA ATTGCTGTTA TGTTTTTAAG AAGCTTATCA     550
TAAGTAATGA GGTTCATGAT TTTTGACATA GTTAGCCTCC GCAGTCTTTC     600
ATTTCAAGTA AATAATAGCG AAATATTCTT TATACTGAAT ACTTATAGTG     650
AAGCAAAGTT CTAGCTTTGA GAAAATTCTT TCTGCAACTA AATATAGTAA     700
ATTACGGTAA AATATAAATA AGTACATATT GAAGAAAATG AGACATAATA     750
TATTTTATAA TAGGAGGGAA TTTCAAATGA TAGACAACTT TATGCAGGTC     800
CTTAAATTAA TTAAAGAGAA ACGTACCAAT AATGTAGTTA AAAAATCTGA     850
TTGGGATAAA GGTGATCTAT ATAAAACTTT AGTCCATGAT AAGTTACCCA     900
AGCAGTTAAA AGTGCATATA AAAGAAGATA AATATTCAGT TGTAGGGAAG     950
GTTGCTACTG GGAACTATAG TAAAGTTCCT TGGATTTCAA TATATGATGA    1000
GAATATAACA AAAGAAACAA AGGATGGATA TTATTTGGTA TATCTTTTTC    1050
ATCCGGAAGG AGAAGGCATA TACTTATCTT TGAATCAAGG ATGGTCAAAG    1100
ATAAGTGATA TGTT                                          1114
```

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1121 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

```
GGAAACTAAA AGAGAAATAT TGGAAGCAAG CCATAGCAGA ATATGAAAAA      50
CGTTTAGGCC CATACACCAA GATAGACATC ATAGAAGTTC CAGACGAAAA     100
AGCACCAGAA AATATGAGCG ACAAAGAAAT TGAGCAAGTA AAAGAAAAAG     150
AAGGCCAACG AATACTAGCC AAAATCAAAC CACAATCCAC AGTCATTACA     200
TTAGAAATAC AAGGAAAGAT GCTATCTTCC GAAGGATTGG CCCAAGAATT     250
GAACCAACGC ATGACCCAAG GGCAAAGCGA CTTTGTATTC GTCATTGGCG     300
GATCAAACGG CCTGCACAAG GACGTCTTAC AACGCAGTAA CTATGCACTA     350
TCATTTAGCA AAATGACATT CCCACATCAA ATGATGCGGG TTGTGTTAAT     400
TGAACAAGTG TATAGAGCAT TTAAGATTAT GCGTGGAGAA GCATATCATA     450
AATGATGCGG TTTTTTCAGC CGCTTCATAA AGGGATTTTG AATGTATCAG     500
AACATATGAG GTTTATGTGA ATTGCTGTTA TGTTTTTAAG AAGCTTATCA     550
TAAGTAATGA GGTTCATGAT TTTTGACATA GTTAGCCTCC GCAGTCTTTC     600
ATTTCAAGTA AATAATAGCG AAATATTCTT TATACTGAAT ACTTATAGTG     650
AAGCAAAGTT CTAGCTTTGA GAAAATTCTT TCTGCAACTA AATATAGTAA     700
```

```
ATTACGGTAA AATATAAATA AGTACATATT GAAGAAAATG AGACATAATA      750
TATTTTATAA TAGGAGGGAA TTTCAAATGA TAGACAACTT TATGCAGGTC      800
CTTAAATTAA TTAAAGAGAA ACGTACCAAT AATGTAGTTA AAAAATCTGA      850
TTGGGATAAA GGTGATCTAT ATAAAACTTT AGTCCATGAT AAGTTACCCA      900
AGCAGTTAAA AGTGCATATA AAAGAAGATA AATATTCAGT TGTAGGGAAG      950
GTTGCTACTG GGAACTATAG TAAAGTTCCT TGGATTTCAA TATATGATGA     1000
GAATATAACA AAAGAAACAA AGGATGGATA TTATTTGGTA TATCTTTTTC     1050
ATCCGGAAGG AGAAGGCATA TACTTATCTT TGAATCAAGG ATGGTCAAAG     1100
ATAAGTGATA TGTTTCCGCG G                                    1121
```

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1121 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

```
TAGCTGTAGG GAAACTAAAA GAGAAATATT GGAAGCAAGC CATAGCAGAA       50
TATGAAAAAC GTTTAGGCCC ATACACCAAG ATAGACATCA TAGAAGTTCC      100
AGACGAAAAA GCACCAGAAA ATATGAGCGA CAAAGAAATT GAGCAAGTAA      150
AAGAAAAAGA AGGCCAACGA ATACTAGCCA AAATCAAACC ACAATCCACA      200
GTCATTACAT TAGAAATACA AGGAAAGATG CTATCTTCCG AAGGATTGGC      250
CCAAGAATTG AACCAACGCA TGACCCAAGG GCAAAGCGAC TTTGTATTCG      300
TCATTGGCGG ATCAAACGGC CTGCACAAGG ACGTCTTACA ACGCAGTAAC      350
TATGCACTAT CATTTAGCAA AATGACATTC CCACATCAAA TGATGCGGGT      400
TGTGTTAATT GAACAAGTGT ATAGAGCATT TAAGATTATG CGTGGAGAAG      450
CATATCATAA ATGATGCGGT TTTTTCAGCC GCTTCATAAA GGGATTTTGA      500
ATGTATCAGA ACATATGAGG TTTATGTGAA TTGCTGTTAT GTTTTTAAGA      550
AGCTTATCAT AAGTAATGAG GTTCATGATT TTTGACATAG TTAGCCTCCG      600
CAGTCTTTCA TTTCAAGTAA ATAATAGCGA AATATTCTTT ATACTGAATA      650
CTTATAGTGA AGCAAAGTTC TAGCTTTGAG AAAATTCTTT CTGCAACTAA      700
ATATAGTAAA TTACGGTAAA ATATAAATAA GTACATATTG AAGAAAATGA      750
GACATAATAT ATTTTATAAT AGGAGGGAAT TTCAAATGAT AGACAACTTT      800
ATGCAGGTCC TTAAATTAAT TAAAGAGAAA CGTACCAATA ATGTAGTTAA      850
AAAATCTGAT TGGGATAAAG GTGATCTATA TAAAACTTTA GTCCATGATA      900
AGTTACCCAA GCAGTTAAAA GTGCATATAA AAGAAGATAA ATATTCAGTT      950
GTAGGGAAGG TTGCTACTGG GAACTATAGT AAAGTTCCTT GGATTTCAAT     1000
ATATGATGAG AATATAACAA AAGAAACAAA GGATGGATAT TATTTGGTAT     1050
ATCTTTTTCA TCCGGAAGGA GAAGGCATAT ACTTATCTTT GAATCAAGGA     1100
TGGTCAAAGA TAAGTGATAT G                                    1121
```

2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

```
CTGTAGGGAA ACTAAAAGAG AAATATTGGA AGCAAGCCAT AGCAGAATAT        50
GAAAAACGTT TAGGCCCATA CACCAAGATA GACATCATAG AAGTTCCAGA       100
CGAAAAAGCA CCAGAAAATA TGAGCGACAA AGAAATTGAG CAAGTAAAAG       150
AAAAAGAAGG CCAACGAATA CTAGCCAAAA TCAAACCACA ATCCACAGTC       200
ATTACATTAG AAATACAAGG AAAGATGCTA TCTTCCGAAG GATTGGCCCA       250
AGAATTGAAC CAACGCATGA CCCAAGGGCA AAGCGACTTT GTATTCGTCA       300
TTGGCGGATC AAACGGCCTG CACAAGGACG TCTTACAACG CAGTAACTAT       350
GCACTATCAT TTAGCAAAAT GACATTCCCA CATCAAATGA TGCGGGTTGT       400
GTTAATTGAA CAAGTGTATA GAGCATTTAA GATTATGCGT GGAGAAGCAT       450
ATCATAAATG ATGCGGTTTT TTCAGCCGCT TCATAAAGGG ATTTTGAATG       500
TATCAGAACA TATGAGGTTT ATGTGAATTG CTGTTATGTT TTTAAGAAGC       550
TTATCATAAG TAATGAGGTT CATGATTTTT GACATAGTTA GCCTCCGCAG       600
TCTTTCATTT CAAGTAAATA ATAGCGAAAT ATTCTTTATA CTGAATACTT       650
ATAGTGAAGC AAAGTTCTAG CTTTGAGAAA ATTCTTTCTG CAACTAAATA       700
TAGTAAATTA CGGTAAAATA TAAATAAGTA CATATTGAAG AAAATGAGAC       750
ATAATATATT TTATAATAGG AGGGAATTTC AAATGATAGA CAACTTTATG       800
CAGGTCCTTA AATTAATTAA AGAGAAACGT ACCAATAATG TAGTTAAAAA       850
ATCTGATTGG GATAAAGGTG ATCTATATAA AACTTTAGTC CATGATAAGT       900
TACCCAAGCA GTTAAAAGTG CATATAAAAG AAGATAAATA TTCAGTTGTA       950
GGGAAGGTTG CTACTGGGAA CTATAGTAAA GTTCCTTGGA TTTCAATATA      1000
TGATGAGAAT ATAACAAAAG AAACAAAGGA TGGATATTAT TTGGTATATC      1050
TTTTTCATCC GGAAGGAGAA GGCATATACT TATCTTTGAA TCAAGGATGG      1100
TCAAAGATAA GTGATATGTT TCCGCGGGAT A                          1131
```

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 896 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

```
CATTAGAAAT ACAAGGAAAG ATGCTATCTT CCGAAGGATT GGCCCAAGAA      50
TTGAACCAAC GCATGACCCA AGGGCAAAGC GACTTTGTAT TCGTCATTGG     100
CGGATCAAAC GGCCTGCACA AGGACGTCTT ACAACGCAGT AACTATGCAC     150
TATCATTTAG CAAAATGACA TTCCCACATC AAATGATGCG GGTTGTGTTA     200
ATTGAACAAG TGTATAGAGC ATTTAAGATT ATGCGTGGAG AAGCATATCA     250
TAAATGATGC GGTTTTTTCA GCCGCTTCAT AAAGGGATTT TGAATGTATC     300
AGAACATATG AGGTTTATGT GAATTGCTGT TATGTTTTTA AGAAGCTTAT     350
CATAAGTAAT GAGGTTCATG ATTTTTGACA TAGTTAGCCT CCGCAGTCTT     400
TCATTTCAAG TAAATAATAG CGAAATATTC TTTATACTGA ATACTTATAG     450
TGAAGCAAAG TTCTAGCTTT GAGAAAATTC TTTCTGCAAC TAAATATAGT     500
AAATTACGGT AAAATATAAA TAAGTACATA TTGAAGAAAA TGAGACATAA     550
TATATTTTAT AATAGGAGGG AATTTCAAAT GATAGACAAC TTTATGCAGG     600
TCCTTAAATT AATTAAAGAG AAACGTACCA ATAATGTAGT TAAAAAATCT     650
GATTGGGATA AAGGTGATCT ATATAAAACT TTAGTCCATG ATAAGTTACC     700
CAAGCAGTTA AAAGTGCATA TAAAAGAAGA TAAATATTCA GTTGTAGGGA     750
AGGTTGCTAC TGGGAACTAT AGTAAAGTTC CTTGGATTTC AATATATGAT     800
GAGAATATAA CAAAAGAAAC AAAGGATGGA TATTATTTGG TATATCTTTT     850
TCATCCGGAA GGAGAAGGCA TATACTTATC TTTGAATCAA GGATGG         896
```

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

```
GGAAACTAAA AGAGAAATAT TGGAAGCAAG CCATATCAGA ATATGAAAAA      50
CGTTTAGGCC CATACACCAA GATAGACATC ATAGAAGTTC CAGACGAAAA     100
AGCACCAGAA AATATGAGCG ACAAAGAAAT CGAGCAAGTA AAAGAAAAAG     150
AAGGCCAACG AATACTAGCC AAAATCAAAC CACAATCAAC AGTCATTACA     200
TTAGAAATAC AAGGAAAGAT GCTATCTTCC GAAGGATTGG CTCAAGAATT     250
GAACCAACGC ATGACCCAAG GGCAAAGCGA CTTTGTATTC GTTATTGGCG     300
GATCAAACGG CCTGCACAAG GACGTCTTAC AACGCAGTAA CTATGCACTA     350
TCATTCAGCA AAATGACATT TCCACATCAG ATGATGCGGG TTGTGTTAAT     400
TGAGCAAGTG TATAGAGCAT TTAAGATTAT GCGTGGGGAA GCATATCATA     450
AATGATGCGG TTTTTTCAGC CGCTTCATAA AGGGATTTTG AATGTATCAG     500
AACATATGAG GTTTATGTGA ATTGCTGTTA TGTTTTTAAG AAGCTTATCA     550
TAAGTAATGA GGTTCATGAT TTTTGACATA GTTAGCCTCC GCAGTCTTTC     600
ATTTCAAGTA AATAATAGCG AAATATTCTT TATACTGAAT ACTTATAGTG     650
AAGCAAAGTT CTAGCTTTGA GAAAATTCTT TCTGCAACTA AATATAGTAA     700
ATTACGGTAA AATATAAATA AGTACATATT GAAGAAAATG AGACATAATA     750
TATTTTATAA TAGGAGGGAA TTTCAAATGA TAGACAACTT TATGCAGGTC     800
CTTAAATTAA TTAAAGAGAA ACGTACCAAT AATGTAGTTA AAAAATCTGA     850
TTGGGATAAA GGTGATCTAT ATAAAACTTT AGTCCATGAT AAGTTACCCA     900
AGCAGTTAAA AGTGCATATA AAAGAAGATA AATATTCAGT TGTAGGGAAG     950
```

```
GTTGCTACTG GGAACTATAG TAAAGTTCCT TGGATTTCAA TATATGATGA      1000
GAATATAACA AAAGAAACAA AGGATGGATA TTATTTGGTA TATCTTTTTC      1050
ATCCGGAAGG AGAAGGCATA TACTTATCTT TGAATCAAGG ATGGTCAAAG      1100
ATAAGTGATA TGTTTCCGCG GGATA                                 1125
```

2) INFORMATION FOR SEQ ID NO: 184

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 679 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

```
ATAAGAGGGA ACAGTGTGAA CAAGTTAATA ACTTGTGGAT AACTGGAAAG       50
TTGATAACAA TTTGGAGGAC CAAACGACAT GAAAATCACC ATTTTAGCTG      100
TAGGGAAACT AAAAGAGAAA TATTGGAAGC AAGCCATAGC AGAATATGAA      150
AAACGTTTAG GCCCATACAC CAAGATAGAC ATCATAGAAG TTCCAGACGA      200
AAAAGCACCA GAAAATATGA GCGACAAAGA AATTGAGCAA GTAAAAGAAA      250
AAGAAGGCCA ACGAATACTA GCCAAAATCA AACCACAATC CACAGTCATT      300
ACATTAGAAA TACAAGGAAA GATGCTATCT TCCGAAGGAT TGGCCCAAGA      350
ATTGAACCAA CGCATGACCC AAGGGCAAAG CGACTTTGTA TTCGTCATTG      400
GCGGATCAAA CGGCCTGCAC AAGGACGTCT TACAACGCAG TAACTATGCA      450
CTATCATTTA GCAAAATGAC ATTCCCACAT CAAATGATGC GGGTTGTGTT      500
AATTGAACAA GTGTATAGAG CATTTAAGAT TATGCGTGGA GAGGCTTATC      550
ATAAATAAAA CTAAAAATTA GATTGTGTAT AATTTAAAAA TTTAATGAGA      600
TGTGGAGGAA TTACATATAT GAAATATTGG AGTATACCTT GCAATATCAT      650
ACGATGTTTA TAGAGTGTTT AATAAACCA                             679
```

2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

```
GGAAACTAAA AGAGAAATAT TGGAAGCAAG CCATAGCAGA ATATGAAAAA      50
CGTTTAGGCC CATACACCAA GATAGACATC ATAGAAGTTC CAGACGAAAA     100
AGCACCAGAA AATATGAGCG ACAAAGAAAT TGAGCAAGTA AAAGAAAAAG     150
AAGGCCAACG AATACTAGCC AAAATCAAAC CACAATCAAC AGTCATTACA     200
TTAGAAATAC AAGGAAAGAT GCTATCTTCC GAAGGATTGG CACAAGAATT     250
GAACCAACGC ATGACCCAAG GGCAAAGCGA CTTTGTATTC GTCATTGGCG     300
GATCAAACGG CCTGCACAAG GACGTCTTAC AACGTAGTAA CTACGCACTA     350
TCATTCAGCA AAATGACATT CCCACATCAA ATGATGCGGG TTGTGTTAAT     400
TGAGCAAGTG TATAGAGCGT TTAAGATTAT GCGTGGAGAA GCATATCATA     450
AATGATGCGG TTTTTTCAGC CGCTTCATAA AGGGATTTTG AATGTATCAG     500
AACATATGAG GTTTATGTGA ATTGCTGTTA TGTTTTTAAG AAGCTTATCA     550
TAAGTAATGA GGTTCATGAT TTTTGACATA GTTAGCCTCC GCAGTCTTTC     600
ATTTCAAGTA AATAATAGCG AAATATTCTT TATACTGAAT ACTTATAGTG     650
AAGCAAAGTT CTAGCTTTGA GAAAATTCTT TCTGCAACTA AATATAGTAA     700
ATTACGGTAA AATATAAATA AGTACATATT GAAGAAAATG AGACATAATA     750
TATTTTATAA TAGGAGGGAA TTTCAAATGA TAGACAACTT TATGCAGGTC     800
CTTAAATTAA TTAAAGAGAA ACGTACCAAT AATGTAGTTA AAAAATCTGA     850
TTGGGATAAA GGTGATCTAT ATAAAACTTT AGTCCATGAT AAGTTACCCA     900
AGCAGTTAAA AGTGCATATA AAAGAAGATA AATATTCAGT TGTAGGGAAG     950
GTTGCTACTG GGAACTATAG TAAAGTTCCT TGGATTTCAA TATATGATGA    1000
GAATATAACA AAAGAAACAA AGGATGGATA TTATTTGGTA TATCTTTTTC    1050
ATCCGGAAGG AGAAGGCATA TACTTATCTT TGAATCAAGG ATGGTCAAAG    1100
ATAAGTGATA TGTTTCCGCG GGATA                               1125
```

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 926 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

```
TACATTAGAA ATACAAGGAA AGATGCTATC TTCCGAAGGA TTGGCCCAAG      50
AATTGAACCA ACGCATGACC CAAGGGCAAA GCGACTTTGT ATTCGTCATT     100
GGCGGATCAA ACGGCCTGCA CAAGGACGTC TTACAACGCA GTAACTATGC     150
ACTATCATTT AGCAAAATGA CATTCCCACA TCAAATGATG CGGGTTGTGT     200
TAATTGAACA AGTGTATAGA GCATTTAAGA TTATGCGTGG AGAAGCATAT     250
CATAAATGAT GCGGTTTTTT CAGCCGCTTC ATAAAGGGAT TTTGAATGTA     300
TCAGAACATA TGAGGTTTAT GTGAATTGCT GTTATGTTTT TAAGAAGCTT     350
ATCATAAGTA ATGAGGTTCA TGATTTTTGA CATAGTTAGC CTCCGCAGTC     400
TTTCATTTCA AGTAAATAAT AGCGAAATAT TCTTTATACT GAATACTTAT     450
AGTGAAGCAA AGTTCTAGCT TTGAGAAAAT TCTTTCTGCA ACTAAATATA     500
GTAAATTACG GTAAAATATA AATAAGTACA TATTGAAGAA AATGAGACAT     550
AATATATTTT ATAATAGGAG GGAATTTCAA ATGATAGACA ACTTTATGCA     600
GGTCCTTAAA TTAATTAAAG AGAAACGTAC CAATAATGTA GTTAAAAAAT     650
CTGATTGGGA TAAAGGTGAT CTATATAAAA CTTTAGTCCA TGATAAGTTA     700
```

```
CCCAAGCAGT TAAAAGTGCA TATAAAAGAA GATAAATATT CAGTTGTAGG      750
GAAGGTTGCT ACTGGGAACT ATAGTAAAGT TCCTTGGATT TCAATATATG      800
ATGAGAATAT AACAAAAGAA ACAAAGGATG GATATTATTT GGTATATCTT      850
TTTCATCCGG AAGGAGAAGG CATATACTTA TCTTTGAATC AAGGATGGTC      900
AAAGATAAGT GATATGTTTC CGCGGG                               926
```

2) INFORMATION FOR SEQ ID NO: 187

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

```
GGATGTGGGT ATGCTAATGT TGTT                                  24
```

2) INFORMATION FOR SEQ ID NO: 188

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188

```
TGAACAATTT TATTTCTCAT ACCATAG                               27
```

2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2154 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

CGGTAATAAA AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC 50
GTAACGATGG TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT 100
TACTTCTCCC TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG 150
ACACTGTAAC GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT 200
TCAGCGATAA CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT 250
AACGTTATTC ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT 300
CTTCTACCCA TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA 350
ATGATACCTT TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT 400
ATATTGAGGA TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA 450
TATGAAGGCT TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT 500
TTCATATATG TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA 550
TGTTAAAGGT AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT 600
TCTATTGAGA CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA 650
TCAACTCCCC AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT 700
CCATACGTTC AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT 750
TAGTAAGTTT GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT 800
AAAAGTGTTC TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC 850
TCTGTTATAT TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT 900
TAAAGCTTGA AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT 950
TCTTCCACTT GCTTAACCAT ACTTTTAGAA AGTGCTAGTC CATTCGGTCC 1000
AGTAATACCT TTTAATTCTA CATTTAAATT CATATTATAT TCATTTGCTA 1050
TTTTTACTAC ATCATCGAAA GTTGGCAAAT GTTCATCTTT GAATTTTTCA 1100
CCAAACCAAG ATCCTGCAGA AGCATCTTTA ATTTCATCAT AATTCAATTC 1150
AGTTATTTCC CCGGACATAT TTGTAGTCCG TTCTAAATAA TCATCATGAA 1200
TGATAATCAG TTGTTCATCT TTTGTAATTG CAACATCTAA CTCCAACCAG 1250
TTTATACCTT CTACTTCTGA AGCAGCTTTA AATGATGCAA TTGTATTTTC 1300
CGGAGCTTTA CTAGGTAATC CTCTATGTCC ATATACAGTT AGCATATTAC 1350
CTCTCCTTGC ATTTTTATTT TTTTAATTAA CGTAACTGTA TTATCACATT 1400
AATCGCACTT TTATTTCCAT TAAAAAGAGA TGAATATCAT AAATAAAGAA 1450
GTCGATAGAT TCGTATTGAT TATGGAGTTA ATCTACGTCT CATCTCATTT 1500
TTAAAAAATC ATTTATGTCC CAAGCTCCAT TTTGTAATCA AGTCTAGTTT 1550
TTCGGTTCTG TTGCAAAGTT GAATTTATAG TATAATTTTA ACAAAAAGGA 1600
GTCTTCTGTA TGAACTATTT CAGATATAAA CAATTTAACA AGGATGTTAT 1650
CACTGTAGCC GTTGGCTACT ATCTAAGATA TACATTGAGT TATCGTGATA 1700
TATCTGAAAT ATTAAGGGAA CGTGGTGTAA ACGTTCATCA TTCAACGGTC 1750
TACCGTTGGG TTCAAGAATA TGCCCCAATT TTGTATCAAA TTTGGAAGAA 1800
AAAGCATAAA AAAGCTTATT ACAAATGGCG TATTGATGAG ACGTACATCA 1850
AAATAAAAGG AAAATGGAGC TATTTATATC GTGCCATTGA TGCAGAGGGA 1900
CATACATTAG ATATTTGGTT GCGTAAGCAA CGAGATAATC ATTCAGCATA 1950
TGCGTTTATC AAACGTCTCA TTAAACAATT TGGTAAACCT CAAAAGGTAA 2000
TTACAGATCA GGCACCTTCA ACGAAGGTAG CAATGGCTAA AGTAATTAAA 2050
GCTTTTAAAC TTAAACCTGA CTGTCATTGT ACATCGAAAT ATCTGAATAA 2100
CCTCATTGAG CAAGATCACC GTCATATTAA AGTAAGAAAG ACAAGGTATC 2150
AAAG 2154

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2410 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA 50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC 100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT 150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG 200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT 250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA 300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT 350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT 400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA 450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT 500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG 550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT 600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT 650
AAATAAAACA CATAAAGAAG ATATTTATAG ATCTTATGCA AACTTAATTG 700
GCAAATCCGG TACTGCAGAA CTCAAAATGA AACAAGGAGA AACTGGCAGA 750
CAAATTGGGT GGTTTATATC ATATGATAAA GATAATCCAA ACATGATGAT 800
GGCTATTAAT GTTAAAGATG TACAAGATAA AGGAATGGCT AGCTACAATG 850
CCAAAATCTC AGGTAAAGTG TATGATGAGC TATATGAGAA CGGTAATAAA 900
AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC GTAACGATGG 950
TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT TACTTCTCCC 1000
TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG ACACTGTAAC 1050
GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT TCAGCGATAA 1100
CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT AACGTTATTC 1150
ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT CTTCTACCCA 1200
TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA ATGATACCTT 1250
TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT ATATTGAGGA 1300
TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA TATGAAGGCT 1350
TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT TTCATATATG 1400
TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA TGTTAAAGGT 1450
AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT TCTATTGAGA 1500
CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA TCAACTCCCC 1550
AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT CCATACGTTC 1600
AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT TAGTAAGTTT 1650
GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT AAAAGTGTTC 1700
TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC TCTGTTATAT 1750
TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT TAAAGCTTGA 1800
AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT TCTTCCACTT 1850
GCTTAACCAT ACTTTTAGAA AGTGCTAGTC CATTCGGTCC AGTAATACCT 1900
TTTAATTCTA CATTTAAATT CATATTATAT TCATTTGCTA TTTTTACTAC 1950
ATCATCGAAA GTTGGCAAAT GTTCATCTTT GAATTTTTCA CCAAACCAAG 2000
ATCCTGCAGA AGCATCTTTA ATTTCATCAT AATTCAATTC AGTTATTTCC 2050
CCGGACATAT TTGTAGTCCG TTCTAAATAA TCATCATGAA TGATAATCAG 2100
TTGTTCATCT TTTGTAATTG CAACATCTAA CTCCAACCAG TTTATACCTT 2150
CTACTTCTGA AGCAGCTTTA AATGATGCAA TTGTATTTTC CGGAGCTTTA 2200
CTAGGTAATC CTCTATGTCC ATATACAGTT AGCATATTAC CTCTCCTTGC 2250
ATTTTTATTT TTTTAATTAA CGTAACTGTA TTATCACATT AATCGCACTT 2300
TTATTTCCAT TAAAAAGAGA TGAATATCAT AAATAAAGAA GTCGATAGAT 2350
TCGTATTGAT TATGGAGTTA ATCTACGTCT CATCTCATTT TTAAAAAATC 2400
ATTTATGTCC 2410

2) INFORMATION FOR SEQ ID NO: 191

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1858 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

```
CACCTTCATA TGACGTCTAT CCATTTATGT ATGGCATGAG TAACGAAGAA      50
TATAATAAAT TAACCGAAGA TAAAAAAGAA CCTCTGCTCA ACAAGTTCCA     100
GATTACAACT TCACCAGGTT CAACTCAAAA AATATTAACA GCAATGATTG     150
GGTTAAATAA CAAAACATTA GACGATAAAA CAAGTTATAA AATCGATGGT     200
AAAGGTTGGC AAAAAGATAA ATCTTGGGGT GGTTACAACG TTACAAGATA     250
TGAAGTGGTA AATGGTAATA TCGACTTAAA ACAAGCAATA GAATCATCAG     300
ATAACATTTT CTTTGCTAGA GTAGCACTCG AATTAGGCAG TAAGAAATTT     350
GAAAAAGGCA TGAAAAAACT AGGTGTTGGT GAAGATATAC CAAGTGATTA     400
TCCATTTTAT AATGCTCAAA TTTCAAACAA AAATTTAGAT AATGAAATAT     450
TATTAGCTGA TTCAGGTTAC GGACAAGGTG AAATACTGAT TAACCCAGTA     500
CAGATCCTTT CAATCTATAG CGCATTAGAA AATAATGGCA ATATTAACGC     550
ACCTCACTTA TTAAAAGACA CGAAAAACAA AGTTTGGAAG AAAAATATTA     600
TTTCCAAAGA AAATATCAAT CTATTAACTG ATGGTATGCA ACAAGTCGTA     650
AATAAAACAC ATAAAGAAGA TATTTATAGA TCTTATGCAA ACTTAATTGG     700
CAAATCCGGT ACTGCAGAAC TCAAAATGAA ACAAGGAGAA ACTGGCAGAC     750
AAATTGGGTG GTTTATATCA TATGATAAAG ATAATCCAAA CATGATGATG     800
GCTATTAATG TTAAAGATGT ACAAGATAAA GGAATGGCTA GCTACAATGC     850
CAAAATCTCA GGTAAAGTGT ATGATGAGCT ATATGAGAAC GGTAATAAAA     900
AATACGATAT AGATGAATAA CAAAACAGTG AAGCAATCCG TAACGATGGT     950
TGCTTCACTG TTTTATTATG AATTATTAAT AAGTGCTGTT ACTTCTCCCT    1000
TAAATACAAT TTCTTCATTT TCATTGTATG TTGAAAGTGA CACTGTAACG    1050
AGTCCATTTT CTTTTTTTAT GGATTTCTTA TTTGTAATTT CAGCGATAAC    1100
GTACAATGTA TTACCTGGGT ATACAGGTTT AATAAATTTA ACGTTATTCA    1150
TTTGTGTTCC TGCTACAACT TCTTCTCCGT ATTTACCTTC TTCTACCCAT    1200
AATTTAAATG ATATTGAAAG TGTATGCATG CCAGATGCAA TGATACCTTT    1250
AAATCTACTT TGTTCTGCTT TTTCTTTATC TATATGCATA TATTGAGGAT    1300
CAAAAGTTGT TGCAAATTGG ATAATTTCTT CTTCTGTAAT ATGAAGGCTT    1350
TTTGTTTTGA ATGTTTCTCC TACTATAAAA TCATCGTATT TCATATATGT    1400
CTCTCTTTCT TATTCAAATT AATTTTTTAG TATGTAACAT GTTAAAGGTA    1450
AGTCTACCGT CACTGAAACG TAAGACTCAC CTCTAACTTT CTATTGAGAC    1500
AAATGCACCA TTTTATCTGC ATTGTCTGTA AAGATACCAT CAACTCCCCA    1550
ATTAGCAAGT TGGTTTGCAC GTGCTGGTTT GTTTACAGTC CATACGTTCA    1600
ATTCATAACC CGCTTCTTTT ACCATTTTTA CTTTTGCTTT AGTAAGTTTG    1650
GCATCTTCAG TGTTTACTAT TTTAGCATTA CAGTAATCTA AAAGTGTTCT    1700
CCAGTCTTCA CGAAACGAAG TTGTATGGAA TATAACTGCT CTGTTATATT    1750
GTGGCATGAT TTCTTCTGCA AGTTTAACAA GCACAACATT AAAGCTTGAA    1800
ATGAGCACTT CTTGATTCTG ATTTAAGTTT GTTAATTGTT CTTCCACTTG    1850
CTTAACCA                                                 1858
```

2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

```
CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA      50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC     100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT     150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG     200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT     250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA     300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT     350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT     400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA     450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT     500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG     550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT     600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT     650
AAATAAAACA CATAAAGAAG ATATTTATAG ATCTTATGCA AACTTAATTG     700
GCAAATCCGG TACTGCAGAA CTCAAAATGA AACAAGGAGA AACTGGCAGA     750
CAAATTGGGT GGTTTATATC ATATGATAAA GATAATCCAA ACATGATGAT     800
GGCTATTAAT GTTAAAGATG TACAAGATAA AGGAATGGCT AGCTACAATG     850
CCAAAATCTC AGGTAAAGTG TATGATGAGC TATATGAGAA CGGTAATAAA     900
AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC GTAACGATGG     950
TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT TACTTCTCCC    1000
TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG ACACTGTAAC    1050
GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT TCAGCGATAA    1100
CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT AACGTTATTC    1150
ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT CTTCTACCCA    1200
TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA ATGATACCTT    1250
TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT ATATTGAGGA    1300
TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA TATGAAGGCT    1350
TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT TTCATATATG    1400
TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA TGTTAAAGGT    1450
AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT TCTATTGAGA    1500
CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA TCAACTCCCC    1550
AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT CCATACGTTC    1600
AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT TAGTAAGTTT    1650
GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT AAAAGTGTTC    1700
TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC TCTGTTATAT    1750
TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT TAAAGCTTGA    1800
AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT TCTTCCACTT    1850
GCTTAACCAT A                                              1861
```

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

```
CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA      50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC     100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT     150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG     200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT     250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA     300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT     350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT     400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA     450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT     500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG     550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT     600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT     650
AAATAAAACA CATAAAGAAG ATATTTATAG ATCTTATGCA AACTTAATTG     700
GCAAATCCGG TACTGCAGAA CTCAAAATGA AACAAGGAGA AACTGGCAGA     750
CAAATTGGGT GGTTTATATC ATATGATAAA GATAATCCAA ACATGATGAT     800
GGCTATTAAT GTTAAAGATG TACAAGATAA AGGAATGGCT AGCTACAATG     850
CCAAAATCTC AGGTAAAGTG TATGATGAGC TATATGAGAA CGGTAATAAA     900
AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC GTAACGATGG     950
TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT TACTTCTCCC    1000
TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG ACACTGTAAC    1050
GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT TCAGCGATAA    1100
CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT AACGTTATTC    1150
ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT CTTCTACCCA    1200
TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA ATGATACCTT    1250
TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT ATATTGAGGA    1300
TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA TATGAAGGCT    1350
TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT TTCATATATG    1400
TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA TGTTAAAGGT    1450
AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT TCTATTGAGA    1500
CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA TCAACTCCCC    1550
AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT CCATACGTTC    1600
AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT TAGTAAGTTT    1650
GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT AAAAGTGTTC    1700
TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC TCTGTTATAT    1750
TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT TAAAGCTTGA    1800
AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT TCTTCCACTT    1850
GCTTAACCAT A                                              1861
```

2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1052 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

```
CGGTAATAAA AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC        50
GTAACGATGG TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT       100
TACTTCTCCC TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG       150
ACACTGTAAC GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT       200
TCAGCGATAA CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT       250
AACGTTATTC ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT       300
CTTCTACCCA TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA       350
ATGATACCTT TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT       400
ATATTGAGGA TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA       450
TATGAAGGCT TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT       500
TTCATATATG TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA       550
TGTTAAAGGT AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT       600
TCTATTGAGA CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA       650
TCAACTCCCC AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT       700
CCATACGTTC AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT       750
TAGTAAGTTT GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT       800
AAAAGTGTTC TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC       850
TCTGTTATAT TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT       900
TAAAGCTTGA AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT       950
TCTTCCACTT GCTTAACCAT ACTTTTAGAA AGTGCTAGTC CATTCGGTCC      1000
AGTAATACCT TTTAATTCTA CATTTAAATT CATATTATAT TCATTTGCTA      1050
TT                                                         1052
```

2) INFORMATION FOR SEQ ID NO: 195

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus

(B) STRAIN: CCRI-9770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

```
CTTCATATGA CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT      50
AATAAATTAA CCGAAGATAA AAAAGAACCT CTGCTCAACA AGTTCCAGAT     100
TACAACTTCA CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT     150
TAAATAACAA AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA     200
GGTTGGCAAA AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA     250
AGTGGTAAAT GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA     300
ACATTTTCTT TGCTAGAGTA GCACTCGAAT TAGGCAGTAA GAAATTTGAA     350
AAAGGCATGA AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC     400
ATTTTATAAT GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT     450
TAGCTGATTC AGGTTACGGA CAAGGTGAAA TACTGATTAA CCCAGTACAG     500
ATCCTTTCAA TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC     550
TCACTTATTA AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT     600
CCAAAGAAAA TATCAATCTA TTAACTGATG GTATGCAACA AGTCGTAAAT     650
AAAACACATA AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA     700
ATCCGGTACT GCAGAACTCA AAATGAAACA AGGAGAAACT GGCAGACAAA     750
TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT     800
ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA     850
AATCTCAGGT AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT     900
ACGATATAGA TGAATAACAA AACAGTGAAG CAATCCGTAA CGATGGTTGC     950
TTCACTGTTT TATTATGAAT TATTAATAAG TGCTGTTACT TCTCCCTTAA    1000
ATACAATTTC TTCATTTTCA TTGTATGTTG AAAGTGACAC TGTAACGAGT    1050
CCATTTTCTT TTTTTATGGA TTTCTTATTT GTAATTTCAG CGATAACGTA    1100
CAATGTATTA CCTGGGTATA CAGGTTTAAT AAATTTAACG TTATTCATTT    1150
GTGTTCCTGC TACAACTTCT TCTCCGTATT TACCTTCTTC TACCCATAAT    1200
TTAAATGATA TTGAAAGTGT ATGCATGCCA GATGCAATGA TACCTTTAAA    1250
TCTACTTTGT TCTGCTTTTT CTTTATCTAT ATGCATATAT TGAGGATCAA    1300
AAGTTGTTGC AAATTGGATA ATTTCTTCTT CTGTAATATG AAGGCTTTTT    1350
GTTTTGAATG TTTCTCCTAC TATAAAATCA TCGTATTTCA TATATGTCTC    1400
TCTTTCTTAT TCAAATTAAT TTTTTAGTAT GTAACATGTT AAAGGTAAGT    1450
CTACCGTCAC TGAAACGTAA GACTCACCTC TAACTTTCTA TTGAGACAAA    1500
TGCACCATTT TATCTGCATT GTCTGTAAAG ATACCATCAA CTCCCCAATT    1550
AGCAAGTTGG TTTGCACGTG CTGGTTTGTT TACAGTCCAT ACGTTCAATT    1600
CATAACCCGC TTCTTTTACC ATTTTTACTT TTGCTTTAGT AAGTTTGGCA    1650
TCTTCAGTGT TTACTATTTT AGCATTACAG TAATCTAAAA GTGTTCTCCA    1700
GTCTTCACGA AACGAAGTTG TATGGAATAT AACTGCTCTG TTATATTGTG    1750
GCATGATTTC TTCTGCAAGT TTAACAAGCA CAACATTAAA GCTTGAAATG    1800
AGCACTTCTT GATTCTGATT TAAGTTTGTT AATTGTTCTT CCACTTGCTT    1850
AACCATACTT TTAGAAAGTG CTAGTCCATT CGGTCCAGTA ATACCTTTTA    1900
ATTCTACATT TAAATTCATA TTATATTCAT TTGCTATTTT TACTACATCA    1950
TCGAAAGTTG GCAAATGTTC ATCTTTGAAT TTTTCACCAA ACCAAGATCC    2000
TGCAGAAGCA TCTTTAATTT CATCATAATT CAATTCAGTT ATTTCCCCGG    2050
ACATATTTGT AGTCCGTTCT AAATAATCAT CATGAATGAT AATCAGTTGT    2100
TCATCTTTTG TAATTGCAAC ATCTAACTCC AACCAGTTTA TACCTTCTAC    2150
TTCTGAAGCA GCTTTAAATG ATGCAATTGT ATTTTCCGGA GCTTTACTAG    2200
GTAATCCTCT ATGTCCATAT ACAGTTAGCA TATTACCTCT CCTTGCATTT    2250
TTATTTTTTT AATTAACGTA ACTGTATTAT CACATTAATC GCACTTTTAT    2300
TTCCATTAAA AAGAGATGAA TATCATAAAT AAAGAAGTCG ATAGATTCGT    2350
ATTGATTATG GAGTTAATCT ACGTCTCATC TCATTTTTAA AAAATCATTT    2400
ATGTCCCAAG CTCCATTTTG TAATCAAGTC TAGTTTTTCG GTTCTGTTGC    2450
AAAGTTGAAT TTATAGTATA ATTTTAACAA AAAGGAGTCT TCTGTATGAA    2500
CTATTTCAGA TATAAACAAT TTAACAAGGA TGTTATCACT GTAGCCGTTG    2550
GCTACTATCT AAGATATACA TTGAGTTATC GTGATATATC TGAAATATTA    2600
AGGGAACGTG GTGTAAACGT TCATCATTCA ACGGTCTACC GTTGGGTTCA    2650
AGAATATGCC CCAATTTTGT ATCAAATTTG GAAGAAAAAG CATAAAAAAG    2700
CTTATTACAA ATGGCGTATT GATGAGACGT ACATCAAAAT AAAAGGAAAA    2750
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TGGAGCTATT TATATCGTGC CATTGATGCA GAGGGACATA CATTAGATAT      2800
TTGGTTGCGT AAGCAACGAG ATAATCATTC AGCATATGCG TTTATCAAAC      2850
GTCTCATTAA ACAATTTGGT AAACCTCAAA AGGTAATTAC AGATCAGGCA      2900
CCTTCAACGA AGGTAGCAAT GGCTAAAGTA ATTAAAGCTT TTAAACTTAA      2950
ACCTGACTGT CATTGTACAT CGAAATATCT GAATAACCTC ATTGAGCAAG      3000
ATCACCGTCA TATTAAAGTA AGAAAGACAA GGTATCAAAG TATCAATACA      3050
GCAAAGAATA CTTTAAAAGG TATTGAATGT ATTTACGCTC TATATAAAAA      3100
G                                                          3101
```

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3506 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

```
CCACCTTCAT ATGACGTCTA TCCATTTATG TATGGCATGA GTAACGAAGA        50
ATATAATAAA TTAACCGAAG ATAAAAAAGA ACCTCTGCTC AACAAGTTCC       100
AGATTACAAC TTCACCAGGT TCAACTCAAA AAATATTAAC AGCAATGATT       150
GGGTTAAATA ACAAAACATT AGACGATAAA ACAAGTTATA AAATCGATGG       200
TAAAGGTTGG CAAAAAGATA AATCTTGGGG TGGTTACAAC GTTACAAGAT       250
ATGAAGTGGT AAATGGTAAT ATCGACTTAA AACAAGCAAT AGAATCATCA       300
GATAACATTT TCTTTGCTAG AGTAGCACTC GAATTAGGCA GTAAGAAATT       350
TGAAAAAGGC ATGAAAAAAC TAGGTGTTGG TGAAGATATA CCAAGTGATT       400
ATCCATTTTA TAATGCTCAA ATTTCAAACA AAAATTTAGA TAATGAAATA       450
TTATTAGCTG ATTCAGGTTA CGGACAAGGT GAAATACTGA TTAACCCAGT       500
ACAGATCCTT TCAATCTATA GCGCATTAGA AAATAATGGC AATATTAACG       550
CACCTCACTT ATTAAAAGAC ACGAAAAACA AAGTTTGGAA GAAAAATATT       600
ATTTCCAAAG AAAATATCAA TCTATTAACT GATGGTATGC AACAAGTCGT       650
AAATAAAACA CATAAAGAAG ATATTTATAG ATCTTATGCA AACTTAATTG       700
GCAAATCCGG TACTGCAGAA CTCAAAATGA AACAAGGAGA AACTGGCAGA       750
CAAATTGGGT GGTTTATATC ATATGATAAA GATAATCCAA ACATGATGAT       800
GGCTATTAAT GTTAAAGATG TACAAGATAA AGGAATGGCT AGCTACAATG       850
CCAAAATCTC AGGTAAAGTG TATGATGAGC TATATGAGAA CGGTAATAAA       900
AAATACGATA TAGATGAATA ACAAAACAGT GAAGCAATCC GTAACGATGG       950
TTGCTTCACT GTTTTATTAT GAATTATTAA TAAGTGCTGT TACTTCTCCC      1000
TTAAATACAA TTTCTTCATT TTCATTGTAT GTTGAAAGTG ACACTGTAAC      1050
GAGTCCATTT TCTTTTTTTA TGGATTTCTT ATTTGTAATT TCAGCGATAA      1100
CGTACAATGT ATTACCTGGG TATACAGGTT TAATAAATTT AACGTTATTC      1150
ATTTGTGTTC CTGCTACAAC TTCTTCTCCG TATTTACCTT CTTCTACCCA      1200
TAATTTAAAT GATATTGAAA GTGTATGCAT GCCAGATGCA ATGATACCTT      1250
TAAATCTACT TTGTTCTGCT TTTTCTTTAT CTATATGCAT ATATTGAGGA      1300
TCAAAAGTTG TTGCAAATTG GATAATTTCT TCTTCTGTAA TATGAAGGCT      1350
TTTTGTTTTG AATGTTTCTC CTACTATAAA ATCATCGTAT TTCATATATG      1400
TCTCTCTTTC TTATTCAAAT TAATTTTTTA GTATGTAACA TGTTAAAGGT      1450
AAGTCTACCG TCACTGAAAC GTAAGACTCA CCTCTAACTT TCTATTGAGA      1500
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CAAATGCACC ATTTTATCTG CATTGTCTGT AAAGATACCA TCAACTCCCC      1550
AATTAGCAAG TTGGTTTGCA CGTGCTGGTT TGTTTACAGT CCATACGTTC      1600
AATTCATAAC CCGCTTCTTT TACCATTTTT ACTTTTGCTT TAGTAAGTTT      1650
GGCATCTTCA GTGTTTACTA TTTTAGCATT ACAGTAATCT AAAAGTGTTC      1700
TCCAGTCTTC ACGAAACGAA GTTGTATGGA ATATAACTGC TCTGTTATAT      1750
TGTGGCATGA TTTCTTCTGC AAGTTTAACA AGCACAACAT TAAAGCTTGA      1800
AATGAGCACT TCTTGATTCT GATTTAAGTT TGTTAATTGT TCTTCCACTT      1850
GCTTAACCAT ACTTTTAGAA AGTGCTAGTC CATTCGGTCC AGTAATACCT      1900
TTTAATTCTA CATTTAAATT CATATTATAT TCATTTGCTA TTTTTACTAC      1950
ATCATCGAAA GTTGGCAAAT GTTCATCTTT GAATTTTTCA CCAAACCAAG      2000
ATCCTGCAGA AGCATCTTTA ATTTCATCAT AATTCAATTC AGTTATTTCC      2050
CCGGACATAT TTGTAGTCCG TTCTAAATAA TCATCATGAA TGATAATCAG      2100
TTGTTCATCT TTTGTAATTG CAACATCTAA CTCCAACCAG TTTATACCTT      2150
CTACTTCTGA AGCAGCTTTA AATGATGCAA TTGTATTTTC CGGAGCTTTA      2200
CTAGGTAATC CTCTATGTCC ATATACAGTT AGCATATTAC CTCTCCTTGC      2250
ATTTTTATTT TTTTAATTAA CGTAACTGTA TTATCACATT AATCGCACTT      2300
TTATTTCCAT TAAAAAGAGA TGAATATCAT AAATAAAGAA GTCGATAGAT      2350
TCGTATTGAT TATGGAGTTA ATCTACGTCT CATCTCATTT TTAAAAAATC      2400
ATTTATGTCC CAAGCTCCAT TTTGTAATCA AGTCTAGTTT TTCTGTACCC      2450
CTTATCTGCA ATTTTACTTA GGATTGCTTT TAACTTACCC CTTATCAGCA      2500
ATTTTACTGA GAACTGCTTT TAACGCACCT CTTATCTGCA ATTTTGCCTA      2550
GAACTGCTTT TAACGTACCT CTTATCTGCA ATTTTACTGA GAACTGCTTT      2600
TAACTTACCC CTTATCAGCA ATTTTGCATG GAATTGCTTT TAACGTACCT      2650
CTTATCTGCA ATTTTACTTA GAACTGCTTT TAACAAACCT CTTATCTGCA      2700
ATTTTACTTA GAACTGCTTT TAACGTACCT CTTATCTGTA ATTTTACTGA      2750
GAACTGCTTT TAACAAACCT CTTATCTGCA ATTTTACTTA GAACTGCTTT      2800
TAACAAACCT CTTATCTGCA ATTTTACTTA GAATTGCTTT TACTATTCCT      2850
CTTATTAGTA TAATCTCAGT AAGAATGCGT ATAAAAATGA AAATTACAAC      2900
CGATTTTGTA AGTGCTGACG CCTGAGGGAA TAGTATGTGC GAGAGACTAA      2950
TGGCTCGAGC CATACCCCTA GGCAAGCATG CACGTACAAA ATCGTAAGAT      3000
AAAAAAATAA GCATATCACT GTAAACTTTA AAAAATCAGT TTAGTGATAT      3050
GCTTATTTAT TTCGAGTTAG GATTTATGTC CCAAGCTCAT CAAGCACAAT      3100
CGGCCACTAG TTTATTTCTC TATCTTATAT GTTCTGATAT GGTCTTCTAT      3150
ACTGTATAAG TATACTTTTG AATATGGATC TTGTGTCAAT TCACGTTCGA      3200
AATCAAATTC TTGATTATCA AATCTGTTAA AGAATGTTTC GTATTCTTCG      3250
ACTGATAATT GCTCTCTAGA TTCTAGCATA TTTAAGTGTT TCTCTTTATC      3300
TAATGCTTTG TCATATCCTT TAACGATTGA ACCACTAAAG ATTTCTCCTA      3350
CTGCTCCTGA ACCATAACTA AATAGACATA CTTTCTCTTC TGGTTGGAAT      3400
GTGTGGTTCT GTAATAACGA AATTAAACTT AAGTATAATG ATCCTGTATA      3450
AATGTTACCA ACATCTCTAT TCCATAATAC GGTTCTGTTG CAAAGTTGAA      3500
TTTATA                                                     3506
```

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 928 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus

(B) STRAIN: CCRI-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

```
TACATTAGAA ATACAAGGAA AGATGCTATC TTCCGAAGGA TTGGCCCAAG        50
AATTGAACCA ACGCATGACC CAAGGGCAAA GCGACTTTGT ATTCGTCATT       100
GGCGGATCAA ACGGCCTGCA CAAGGACGTC TTACAACGCA GTAACTACGC       150
ACTATCATTC AGCAAAATGA CATTCCCACA TCAAATGATG CGGGTTGTGT       200
TAATTGAACA AGTGTACAGA GCATTTAAGA TTATGCGTGG AGAAGCATAT       250
CATAAATGAT GCGGTTTTTT CAGCCGCTTC ATAAAGGGAT TTTGAATGTA       300
TCAGAACATA TGAGGTTTAT GTGAATTGCT GTTATGTTTT TAAGAAGCTT       350
ATCATAAGTA ATGAGGTTCA TGATTTTTGA CATAGTTAGC CTCCGCAGTC       400
TTTCATTTCA AGTAAATAAT AGCGAAATAT TCTTTATACT GAATACTTAT       450
AGTGAAGCAA AGTTCTAGCT TTGAGAAAAT TCTTTCTGCA ACTAAATATA       500
GTAAATTACG GTAAAATATA AATAAGTACA TATTGAAGAA AATGAGACAT       550
AATATATTTT ATAATAGGAG GGAATTTCAA ATGATAGACA ACTTTATGCA       600
GGTCCTTAAA TTAATTAAAG AGAAACGTAC CAATAATGTA GTTAAAAAAT       650
CTGATTGGGA TAAAGGTGAT CTATATAAAA CTTTAGTCCA TGATAAGTTA       700
CCCAAGCAGT TAAAAGTGCA TATAAAAGAA GATAAATATT CAGTTGTAGG       750
GAAGGTTGCT ACTGGGAACT ATAGTAAAGT TCCTTGGATT TCAATATATG       800
ATGAGAATAT AACAAAAGAA ACAAAGGATG GATATTATTT GGTATATCTT       850
TTTCATCCGG AAGGAGAAGG CATATACTTA TCTTTGAATC AAGGATGGTC       900
AAAGATAAGT GATATGTTTC CGCGGGAT                               928
```

2) INFORMATION FOR SEQ ID NO: 198

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 782 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

```
CAATGCCCAC AGAGTTATCC ACAAATACAC AGGTTATACA CTAAAAATTG        50
GGCATGAATG TCAGAAAAAT ATCAAAAACT GCAAAGAATA TTGGTATAAT       100
AAGAGGGAAC AGTGTGAACA AGTTAATAAC TTGTGGATAA CTGGAAAGTT       150
GATAACAATT TGGAGGACCA AACGACATGA AAATCACCAT TTTAGCTGTA       200
GGGAAACTAA AAGAGAAATA TTGGAAGCAA GCCATAGCAG AATATGAAAA       250
ACGTTTAGGC CCATACACCA AGATAGACAT CATAGAAGTT CCAGACGAAA       300
AAGCACCAGA AAATATGAGC GACAAAGAAA TTGAGCAAGT AAAAGAAAAA       350
GAAGGCCAAC GAATACTAGC CAAAATCAAA CCACAATCAA CAGTCATTAC       400
ATTAGAAATA CAAGGAAAGA TGCTATCTTC CGAAGGATTG GCCCAAGAAT       450
TGAACCAACG CATGACCCAA GGGCAAAGCG ACTTTGTATT CGTCATTGGC       500
GGATCAAACG GCCTGCACAA GGACGTCTTA CAACGCAGTA ACTACGCACT       550
ATCATTCAGC AAAATGACAT TCCCACATCA AATGATGCGG GTTGTGTTAA       600
TTGAACAAGT GTACAGAGCA TTTAAGATTA TGCGTGGAGA AGCGTATCAT       650
AAATAAAACT AAAAATTAGG TTGTGTATAA TTTAAAAATT TAATGAGATG       700
```

TGGAGGAATT ACATATATGA AATATTGGAT TATACCTTGC AATATCATAC 750
GATGTTTATA GAGTGTTTAA TAAACCATTT TT 782

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 709 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-8894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

TACATTAGAA ATACAAGGAA AGATGCTATC TTCCGAAGGA TTGGCCCAAG 50
AATTGAACCA ACGCATGACC CAAGGGCAAA GCGACTTTGT TTTCGTCATT 100
GGCGGATCAA ACGGCCTGCA CAAGGACGTC TTACAACGCA GTAACTACGC 150
ACTATCATTC AGCAAAATGA CATTCCCACA TCAAATGATG CGGGTTGTGT 200
TAATTGAACA AGTGTACAGA GCATTTAAGA TTATGCGAGG AGAAGCTTAT 250
CATAAGTAAT GAGGTTCATG ATTTTTGACA TAGTTAGCCT CCGCAGTCTT 300
TCATTTCAAG TAAATAATAG CGAAATATTC TTTATACTGA ATACTTATAG 350
TGAAGCAAAG TTCTAGCTTT GAGAAAATTC TTTCTGCAAC TAAATATAGT 400
AAATTACGGT AAAATATAAA TAAGTACATA TTGAAGAAAA TGAGACATAA 450
TATATTTTAT AATAGGAGGG AATTTCAAAT GATAGACAAC TTTATGCAGG 500
TCCTTAAATT AATTAAAGAG AAACGTACCA ATAATGTAGT TAAAAAATCT 550
GATTGGGATA AAGGTGATCT ATATAAAACT TTAGTCCATG ATAAGTTACC 600
CAAGCAGTTA AAAGTGCATA TAAAAGAAGA TAAATATTCA GTTGTAGGGA 650
AGGTTGCTAC TGGGAACTAT AGTAAAGTTC CTTGGATTTC AATATATGAT 700
GAGAATATA 709

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

GTGGGAAATG GCTGTTGTTG AG 22

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

TTCGTTCCCT CCATTAACTG TC 22

2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

AAAAGAAAGA CGGTGAAGGC 20

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CACTTCATTA TACTGTTTTC TTTGC 25

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

TCACCGTCTT TCTTTTGACC TT 22

2) INFORMATION FOR SEQ ID NO: 205

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

TGAGATCTGC TGGAACAAAA GTGAA 25

2) INFORMATION FOR SEQ ID NO: 206

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

CGGTCGAGTT TGCTGAAGAA 20

2) INFORMATION FOR SEQ ID NO: 207

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

TCCCCTAATG ATAGCTGGTA TATATT 26

2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

TCTAGGGAAT CAAAGAAAAG TAATAGT 27

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

CAACAARGRC AATGTGAYRT ATTATGYTGT TA 32

2) INFORMATION FOR SEQ ID NO: 210

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

GATAAYATWG GMGAACAAGT CARAAATGG 29

2) INFORMATION FOR SEQ ID NO: 211

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

CCRTATTGAT TGWTRACACG RCCACARTAA TTWGG 35

2) INFORMATION FOR SEQ ID NO: 212

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

ATRTTSARTG GTTCATTTTT GAAATAGATI CC 32

2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

ACGTGTCGGT ATCTATGTWC GTGTATCAAC RG 32

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

TGTTATGRTC TACAAAACAA ACCGAYTAGC 30

2) INFORMATION FOR SEQ ID NO: 215

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

GAWTAATAAT RGGGGAATGC TTACCTTCAG CTAT 34

2) INFORMATION FOR SEQ ID NO: 216

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

GGTTTTTGAC TGACTTGTTT TTTACG 26

2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

TAGAAYTGTT TTTTATGATT ACCRTCTTT 29

2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

GGCAAAAAYA AAGACGAAGT GCTGAG 26

2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 721 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

```
TGTAGCTTTA GGTGAAGGGT TAGGTCCTTC AATAGGGGGA ATAATAGCAC      50
ATTATATTCA TTGGTCTTAC CTACTTATAC TTCCTATGAT TACAATAGTA     100
ACTATACCTT TTCTTATTAA AGTAATGGTA CCTGGTAAAT CAACAAAAAA     150
TACATTAGAT ATCGTAGGTA TTGTTTTAAT GTCTATAAGT ATTATATGTT     200
TTATGTTATT TACGACAAAT TATAATTGGA CTTTTTTAAT ACTCTTCACA     250
ATCTTTTTTG TGATTTTTAT TAAACATATT TCAAGAGTTT CTAACCCTTT     300
TATTAATCCT AAACTAGGGA AAAACATTCC GTTTATGCTT GGTTTGTTTT     350
CTGGTGGGCT AATATTTTCT ATAGTAGCTG GTTTTATATC AATGGTGCCT     400
TATATGATGA AAACTATTTA TCATGTAAAT GTAGCGACAA TAGGTAATAG     450
```

```
TGTTATTTTT CCTGGAACCA TGAGTGTTAT TGTTTTTGGT TATTTTGGTG      500
GTTTTTTAGT GGATAGAAAA GGATCATTAT TTGTTTTTAT TTTAGGATCA      550
TTGTCTATCT CTATAAGTTT TTTAACTATT GCATTTTTTG TTGAGTTTAG      600
TATGTGGTTG ACTACTTTTA TGTTTATATT TGTTATGGGC GGATTATCTT      650
TTACTAAAAC AGTTATATCA AAAATAGTAT CAAGTAGTCT TTCTGAAGAA      700
GAAGTTGCTT CTGGAAGAGT T                                     721
```

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

```
ATCCGGTACT GCAGAACTCA AAATGAAACA AGGAGAAACT GGCAGACAAA       50
TTGGGTGGTT TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT      100
ATTAATGTTA AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA      150
AATCTCAGGT AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT      200
ACGATATAGA TGAATAACAA AACAGTGAAG CAATCCGTAA CGATGGTTGC      250
TTCACTGTTT TATTATGAAT TATTAATAAG TGCTGTTACT TCTCCCTTAA      300
ATACAATTTC TTCATTTTCA TTGTATGTTG AAAGTGACAC TGTAACGAGT      350
CCATTTTCTT TTTTTATGGA TTTCTTATTT GTAATTTCAG CGATAACGTA      400
CAATGTATTA CCTGGGTATA CAGGTTTAAT AAATTTAACG TTATTCATTT      450
GTGTTCCTGC TACAACTTCT TCTCCGTATT TACCTTCTTC TACCCATAAT      500
TTAAATGATA TTGAAAGTGT ATGCATGCCA GATGCAATGA TACCTTTAAA      550
TCTACTTTGT TCTGCTTTTT CTTTATCTAT ATGCATATAT TGAGGATCAA      600
AAGTTGTTGC AAATTGGATA ATTTCTTCTT CTGTAATATG AAGGCTTTTT      650
GTTTTGAATG TTTCTCCTAC TATAAAATCA TCGTATTTCA TATATGTCTC      700
TCTTTCTTAT TCAAATTAAT TTTTTAGTAT GTAACATGTT AAAGGTAAGT      750
CTACCGTCAC TGAAACGTAA GACTCACCTC TAACTTTCTA TTGAGACAAA      800
TGCACCATTT TATCTGCATT GTCTGTAAAG ATACCATCAA CTCCCCAATT      850
AGCAAGTTGG TTTGCACGTG CTGGTTTGTT TACAGTCCAT ACGTTCAATT      900
CATAACCCGC TTCTTTTACC ATTTTTACTT TTGCTTTAGT AAGTTTGGCA      950
TCTTCAGTGT TTACTATTTT AGCATTACAG TAATCTAAAA GTGTTCTCCA     1000
GTCTTCACGA AACGAAGTTG TATGGAATAT AACTGCTCTG TTATATTGTG     1050
GCATGATTTC TTCTGCAAGT TTAACAAGCA CAACATTAAA GCTTGAAATG     1100
AGCACTTCTT GATTCTGATT TAAGTTTGTT AATTGTTCTT CCACTTGCTT     1150
AACCATACTT TTAGAAAGTG CTAGTCCATT CGGTCCAGTA ATACCTTTTA     1200
ATTCTACATT TAAATTCATA TTATATTCAT TTGCTATTTT TACTACATCA     1250
TCGAAAGTTG GCAAATGTTC ATCTTTGAAT TTTTCACCAA ACCAAGATCC     1300
TGCAGAAGCA TCTTTAATTT CATCATAATT CAATTCAGTT ATTTCCCCGG     1350
ACATATTTGT AGTCCGTTCT AAATAATCAT CATGAATGAT AATCAGTTGT     1400
TCATCTTTTG TAATTGCAAC ATCTAACTCC AACCAGTTTA TACCTTCTAC     1450
TTCTGAAGCA GCTTTAAATG ATGCAATTGT ATTTTCCGGA GCTTTACTAG     1500
GTAATCCTCT ATGTCCATAT ACAGTTAGCA TATTACCTCT CCTTGCATTT     1550
TTATTTTTTT AATTAACGTA ACTGTATTAT CACATTAATC GCACTTTTAT     1600
```

```
TTCCATTAAA AAGAGATGAA TATCATAAAT AAAGAAGTCG ATAGATTCGT      1650
ATTGATTATG GAGTTAATCT ACGTCTCATC TCATTTTTAA AAAATCATTT      1700
ATGTCCCAAG CTCCATTTTG TAATCAAGTC TAGTTTTTCT GTACCCCTTA      1750
TCTGCAATTT TACTTAGGAT TGCTTTTAAC TTACCCCTTA T               1791
```

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 600 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

```
AAGTGCTGAC GCCTGAGGGA ATAGTATGTG CGAGAGACTA ATGGCTCGAG       50
CCATACCCCT AGGCAAGCAT GCACGTACAA AATCGTAAGA TAAAAAAATA      100
AGCATATCAC TGTAAACTTT AAAAAATCAG TTTAGTGATA TGCTTATTTA      150
TTTCGAGTTA GGATTTATGT CCCAAGCTCA TCAAGCACAA TCGGCCACTA      200
GTTTATTTCT CTATCTTATA TGTTCTGATA TGGTCTTCTA TACTGTATAA      250
GTATACTTTT GAATATGGAT CTTGTGTCAA TTCACGTTCG AAATCAAATT      300
CTTGATTATC AAATCTGTTA AAGAATGTTT CGTATTCTTC GACTGATAAT      350
TGCTCTCTAG ATTCTAGCAT ATTTAAGTGT TTCTCTTTAT CTAATGCTTT      400
GTCATATCCT TTAACGATTG AACCACTAAA GATTTCTCCT ACTGCTCCTG      450
AACCATAACT AAATAGACAT ACTTTCTCTT CTGGTTGGAA TGTGTGGTTC      500
TGTAATAACG AAATTAAACT TAAGTATAAT GATCCTGTAT AAATGTTACC      550
AACATCTCTA TTCCATAATA CGGTTCTGTT GCAAAGTTGA ATTTATAGTA      600
```

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1640 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

```
GGGTGGTTTA TATCATATGA TAAAGATAAT CCAAACATGA TGATGGCTAT        50
TAATGTTAAA GATGTACAAG ATAAAGGAAT GGCTAGCTAC AATGCCAAAA       100
TCTCAGGTAA AGTGTATGAT GAGCTATATG AGAACGGTAA TAAAAAATAC       150
GATATAGATG AATAACAAAA CAGTGAAGCA ATCCGTAACG ATGGTTGCTT       200
CACTGTTTTA TTATGAATTA TTAATAAGTG CTGTTACTTC TCCCTTAAAT       250
ACAATTTCTT CATTTTCATT GTATGTTGAA AGTGACACTG TAACGAGTCC       300
ATTTTCTTTT TTTATGGATT TCTTATTTGT AATTTCAGCG ATAACGTACA       350
ATGTATTACC TGGGTATACA GGTTTAATAA ATTTAACGTT ATTCATTTGT       400
GTTCCTGCTA CAACTTCTTC TCCGTATTTA CCTTCTTCTA CCCATAATTT       450
AAATGATATT GAAAGTGTAT GCATGCCAGA TGCAATGATA CCTTTAAATC       500
TACTTTGTTC TGCTTTTTCT TTATCTATAT GCATATATTG AGGATCAAAA       550
GTTGTTGCAA ATTGGATAAT TTCTTCTTCT GTAATATGAA GGCTTTTTGT       600
TTTGAATGTT TCTCCTACTA TAAAATCATC GTATTTCATA TATGTCTCTC       650
TTTCTTATTC AAATTAATTT TTTAGTATGT AACATGTTAA AGGTAAGTCT       700
ACCGTCACTG AAACGTAAGA CTCACCTCTA ACTTTCTATT GAGACAAATG       750
CACCATTTTA TCTGCATTGT CTGTAAAGAT ACCATCAACT CCCCAATTAG       800
CAAGTTGGTT TGCACGTGCT GGTTTGTTTA CAGTCCATAC GTTCAATTCA       850
TAACCCGCTT CTTTTACCAT TTTTACTTTT GCTTTAGTAA GTTTGGCATC       900
TTCAGTGTTT ACTATTTTAG CATTACAGTA ATCTAAAAGT GTTCTCCAGT       950
CTTCACGAAA CGAAGTTGTA TGGAATATAA CTGCTCTGTT ATATTGTGGC      1000
ATGATTTCTT CTGCAAGTTT AACAAGCACA ACATTAAAGC TTGAAATGAG      1050
CACTTCTTGA TTCTGATTTA AGTTTGTTAA TTGTTCTTCC ACTTGCTTAA      1100
CCATACTTTT AGAAAGTGCT AGTCCATTCG GTCCAGTAAT ACCTTTTAAT      1150
TCTACATTTA AATTCATATT ATATTCATTT GCTATTTTTA CTACATCATC      1200
GAAAGTTGGC AAATGTTCAT CTTTGAATTT TTCACCAAAC CAAGATCCTG      1250
CAGAAGCATC TTTAATTTCA TCATAATTCA ATTCAGTTAT TTCCCCGGAC      1300
ATATTTGTAG TCCGTTCTAA ATAATCATCA TGAATGATAA TCAGTTGTTC      1350
ATCTTTTGTA ATTGCAACAT CTAACTCCAA CCAGTTTATA CCTTCTACTT      1400
CTGAAGCAGC TTTAAATGAT GCAATTGTAT TTTCCGGAGC TTTACTAGGT      1450
AATCCTCTAT GTCCATATAC AGTTAGCATA TTACCTCTCC TTGCATTTTT      1500
ATTTTTTTAA TTAACGTAAC TGTATTATCA CATTAATCGC ACTTTTATTT      1550
CCATTAAAAA GAGATGAATA TCATAAATAA AGAAGTCGAT AGATTCGTAT      1600
TGATTATGGA GTTAATCTAC GTCTCATCTC ATTTTTAAAA                 1640
```

2) INFORMATION FOR SEQ ID NO: 223

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 592 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

```
AATTCAACTT TGCAACAGAA CCGTATTATG GAATAGAGAT GTTGGTAACA        50
TTTATACAGG ATCATTATAC TTAAGTTTAA TTTCGTTATT ACAGAACCAC       100
ACATTCCAAC CAGAAGAGAA AGTATGTCTA TTTAGTTATG GTTCAGGAGC       150
AGTAGGAGAA ATCTTTAGTG GTTCAATCGT TAAAGGATAT GACAAAGCAT       200
TAGATAAAGA GAAACACTTA AATATGCTAG AATCTAGAGA GCAATTATCA       250
```

```
GTCGAAGAAT ACGAAACATT CTTTAACAGA TTTGATAATC AAGAATTTGA      300
TTTCGAACGT GAATTGACAC AAGATCCATA TTCAAAAGTA TACTTATACA      350
GTATAGAAGA CCATATCAGA ACATATAAGA TAGAGAAATA AACTAGTGGC      400
CGATTGTGCT TGATGAGCTT GGGACATAAA TCCTAACTCG AAATAAATAA      450
GCATATCACT AAACTGATTT TTTAAAGTTT ACAGTGATAT GCTTATTTTT      500
TTATCTTACG ATTTTGTACG TGCATGCTTG CCTAGGGGTA TGGCTCGAGC      550
CATTAGTCTC TCGCACATAC TATTCCCTCA GGCGTCAGCA CT              592
```

2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2386 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

```
CACCTTCATA TGACGTCTAT CCATTTATGT ATGGCATGAG TAACGAAGAA       50
TATAATAAAT TAACCGAAGA TAAAAAAGAA CCTCTGCTCA ACAAGTTCCA      100
GATTACAACT TCACCAGGTT CAACTCAAAA AATATTAACA GCAATGATTG      150
GGTTAAATAA CAAAACATTA GACGATAAAA CAAGTTATAA AATCGATGGT      200
AAAGGTTGGC AAAAAGATAA ATCTTGGGGT GGTTACAACG TTACAAGATA      250
TGAAGTGGTA AATGGTAATA TCGACTTAAA ACAAGCAATA GAATCATCAG      300
ATAACATTTT CTTTGCTAGA GTAGCACTCG AATTAGGCAG TAAGAAATTT      350
GAAAAAGGCA TGAAAAAACT AGGTGTTGGT GAAGATATAC CAAGTGATTA      400
TCCATTTTAT AATGCTCAAA TTTCAAACAA AAATTTAGAT AATGAAATAT      450
TATTAGCTGA TTCAGGTTAC GGACAAGGTG AAATACTGAT TAACCCAGTA      500
CAGATCCTTT CAATCTATAG CGCATTAGAA AATAATGGCA ATATTAACGC      550
ACCTCACTTA TTAAAAGACA CGAAAAACAA AGTTTGGAAG AAAAATATTA      600
TTTCCAAAGA AAATATCAAT CTATTAACTG ATGGTATGCA ACAAGTCGTA      650
AATAAAACAC ATAAAGAAGA TATTTATAGA TCTTATGCAA ACTTAATTGG      700
CAAATCCGGT ACTGCAGAAC TCAAAATGAA ACAAGGAGAA ACTGGCAGAC      750
AAATTGGGTG GTTTATATCA TATGATAAAG ATAATCCAAA CATGATGATG      800
GCTATTAATG TTAAAGATGT ACAAGATAAA GGAATGGCTA GCTACAATGC      850
CAAAATCTCA GGTAAAGTGT ATGATGAGCT ATATGAGAAC GGTAATAAAA      900
AATACGATAT AGATGAATAA CAAAACAGTG AAGCAATCCG TAACGATGGT      950
TGCTTCACTG TTTTATTATG AATTATTAAT AAGTGCTGTT ACTTCTCCCT     1000
TAAATACAAT TTCTTCATTT TCATTGTATG TTGAAAGTGA CACTGTAACG     1050
AGTCCATTTT CTTTTTTTAT GGATTTCTTA TTTGTAATTT CAGCGATAAC     1100
GTACAATGTA TTACCTGGGT ATACAGGTTT AATAAATTTA ACGTTATTCA     1150
TTTGTGTTCC TGCTACAACT TCTTCTCCGT ATTTACCTTC TTCTACCCAT     1200
AATTTAAATG ATATTGAAAG TGTATGCATG CCAGATGCAA TGATACCTTT     1250
AAATCTACTT TGTTCTGCTT TTTCTTTATC TATATGCATA TATTGAGGAT     1300
CAAAAGTTGT TGCAAATTGG ATAATTTCTT CTTCTGTAAT ATGAAGGCTT     1350
TTTGTTTTGA ATGTTTCTCC TACTATAAAA TCATCGTATT TCATATATGT     1400
CTCTCTTTCT TATTCAAATT AATTTTTTAG TATGTAACAT GTTAAAGGTA     1450
AGTCTACCGT CACTGAAACG TAAGACTCAC CTCTAACTTT CTATTGAGAC     1500
AAATGCACCA TTTTATCTGC ATTGTCTGTA AAGATACCAT CAACTCCCCA     1550
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ATTAGCAAGT TGGTTTGCAC GTGCTGGTTT GTTTACAGTC CATACGTTCA      1600
ATTCATAACC CGCTTCTTTT ACCATTTTTA CTTTTGCTTT AGTAAGTTTG      1650
GCATCTTCAG TGTTTACTAT TTTAGCATTA CAGTAATCTA AAAGTGTTCT      1700
CCAGTCTTCA CGAAACGAAG TTGTATGGAA TATAACTGCT CTGTTATATT      1750
GTGGCATGAT TTCTTCTGCA AGTTTAACAA GCACAACATT AAAGCTTGAA      1800
ATGAGCACTT CTTGATTCTG ATTTAAGTTT GTTAATTGTT CTTCCACTTG      1850
CTTAACCATA CTTTTAGAAA GTGCTAGTCC ATTCGGTCCA GTAATACCTT      1900
TTAATTCTAC ATTTAAATTC ATATTATATT CATTTGCTAT TTTTACTACA      1950
TCATCGAAAG TTGGCAAATG TTCATCTTTG AATTTTTCAC CAAACCAAGA      2000
TCCTGCAGAA GCATCTTTAA TTTCATCATA ATTCAATTCA GTTATTTCCC      2050
CGGACATATT TGTAGTCCGT TCTAAATAAT CATCATGAAT GATAATCAGT      2100
TGTTCATCTT TTGTAATTGC AACATCTAAC TCCAACCAGT TTATACCTTC      2150
TACTTCTGAA GCAGCTTTAA ATGATGCAAT TGTATTTTCC GGAGCTTTAC      2200
TAGGTAATCC TCTATGTCCA TATACAGTTA GCATATTACC TCTCCTTGCA      2250
TTTTTATTTT TTTAATTAAC GTAACTGTAT TATCACATTA ATCGCACTTT      2300
TATTTCCATT AAAAAGAGAT GAATATCATA AATAAAGAAG TCGATAGATT      2350
CGTATTGATT ATGGAGTTAA TCTACGTCTC ATCTCA                     2386
```

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 623 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

```
TGAAAATTAC AACCGATTTT GTAAGTGCTG ACGCCTGAGG GAATAGTATG        50
TGCGAGAGAC TAATGGCTCG AGCCATACCC CTAGGCAAGC ATGCACGTAC       100
AAAATCGTAA GATAAAAAAA TAAGCATATC ACTGTAAACT TTAAAAAATC       150
AGTTTAGTGA TATGCTTATT TATTTCGAGT TAGGATTTAT GTCCCAAGCT       200
CATCAAGCAC AATCGGCCAC TAGTTTATTT CTCTATCTTA TATGTTCTGA       250
TATGGTCTTC TATACTGTAT AAGTATACTT TTGAATATGG ATCTTGTGTC       300
AATTCACGTT CGAAATCAAA TTCTTGATTA TCAAATCTGT TAAAGAATGT       350
TTCGTATTCT TCGACTGATA ATTGCTCTCT AGATTCTAGC ATATTTAAGT       400
GTTTCTCTTT ATCTAATGCT TTGTCATATC CTTTAACGAT TGAACCACTA       450
AAGATTTCTC CTACTGCTCC TGAACCATAA CTAAATAGAC ATACTTTCTC       500
TTCTGGTTGG AATGTGTGGT TCTGTAATAA CGAAATTAAA CTTAAGTATA       550
ATGATCCTGT ATAAATGTTA CCAACATCTC TATTCCATAA TACGGTTCTG       600
TTGCAAAGTT GAATTTATAG TAT                                   623
```

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(C) ACCESSION NUMBER: Extracted from L29436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

```
ATGAAAAATA TTTCAGAATT CTCAGCCCAA CTTGATCAAA CTTTTGATCA        50
AGGGGAAGCC GTCTCTATGG AGTGGTTATT CCGTCCGTTG CTAAAAATGC       100
TGGCGGAGGG CGATCCAGTC CCCGTTGAGG ACATCGCGGC GGAGACCGGG       150
AAGCCCGTCG AGGAAGTTAA GCAAGTCCTA CAGACTCTAC CTAGTGTGGA       200
ACTTGATGAG CAGGGCCGTG TCGTCGGTTA TGGCCTCACA CTGTTCCCTA       250
CCCCCCATCG CTTCGAGGTT GATGGGAAGC AACTATATGC ATGGTGCGCC       300
CTTGACACAC TTATGTTCCC AGCACTCATC GGCCGGACGG TCCACATCGC       350
TTCGCCTTGT CACGGCACCG GTAAGTCCGT CCGGTTGACG GTGGAACCGG       400
ACCGCGTTGT AAGCGTCGAG CCTTCAACAG CCGTTGTCTC GATTGTTACA       450
CCAGATGAAA TGGCCTCGGT TCGGTCGGCC TTCTGTAACG ACGTTCACTT       500
TTTCAGTTCA CCGAGTGCAG CCCAAGACTG GCTTAACCAA CACCCTGAGT       550
CGAGCGTTTT GCCCGTTGAA GATGCCTTTG AACTGGGTCG CCATTTGGGA       600
GCGCGTTATG AGGAGTCAGG ACCTACTAAT GGGTCCTGTT GTAACATTTA       650
A                                                           651
```

2) INFORMATION FOR SEQ ID NO: 227

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 563 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(C) ACCESSION NUMBER: Extracted from L29436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

```
ATGAATCTTG AAAAAGGGAA TATAGAAAGG AAAAAACATG GTGTCCATGT        50
TAATGAGTAT TTGCAAAGTG TAAGTAACCC GAATGTCTAT GCAGCTGGAG       100
ATGCTGCAGC AACGGATGGC TTGCCCCTCA CACCTGTAGC CAGTGCAGAT       150
TCTCATGTCG TAGCATCTAA TTTATTGAAA GGGAACAGCA AAAAAATTGA       200
ATATCCCGTG ATTCCATCTG CTGTATTTAC CGTACCTAAA ATGGCATCGG       250
TAGGTATGAG CGAGGAGGAA GCCAAAAACT CTGGCCGGAA TATTAAAGTA       300
AAGCAGAAAA ACATCTCCGA CTGGTTTACG TATAAACGGA CAAATGAGGA       350
CTTTGCTGCG TTTAAAGTGC TGATTGACGA AGATCATGAT CAAATTGTTG       400
GTGCTCATTT GATTAGTAAT GAAGCCGATG AACTGATTAA TCATTTTGCA       450
ACAGCCATTC GTTTTGGGAT TTCAACCAAA GAATTGAAAC AAATGATATT       500
```

TGCCTATCCA ACGGCAGCTT CGGACATTGC ACACATGTTG TAAGTTTGCG 550
TTTTGTGAGA TGT 563

2) INFORMATION FOR SEQ ID NO: 228

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(C) ACCESSION NUMBER: Extracted from S67449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TTGTTTAGTT TATATAAAAA ATTTAAAGGT TTGTTTTATA GCGTTTTATT 50
TTGGCTTTGT ATTCTTTCAT TTTTTAGTGT ATTAAATGAA ATGGTTTTAA 100
ATGTTTCTTT ACCTGATATT GCAAATCATT TTAATACTAC TCCTGGAATT 150
ACAAACTGGG TAAACACTGC ATATATGTTA ACTTTTTCGA TAGGAACAGC 200
AGTATATGGA AAATTATCTG ATTATATAAA TATAAAAAAA TTGTTAATTA 250
TTGGTATTAG TTTGAGCTGT CTTGGTTCAT TGATTGCTTT TATTGGTCAC 300
AATCACTTTT TTATTTTGAT TTTTGGTAGG TTAGTACAAG GAGTAGGATC 350
TGCTGCATTC CCTTCACTGA TTATGGTGGT TGTAGCTAGA AATATTACAA 400
GAAAAAAACA AGGCAAAGCC TTTGGTTTTA TAGGATCAAT TGTAGCTTTA 450
GGTGAAGGGT TAGGTCCTTC AATAGGGGGA ATAATAGCAC ATTATATTCA 500
TTGGTCTTAC CTACTTATAC TTCCTATGAT TACAATAGTA ACTATACCTT 550
TTCTTATTAA AGTAATGGTA CCTGGTAAAT CAACAAAAAA TACATTAGAT 600
ATCGTAGGTA TTGTTTTAAT GTCTATAAGT ATTATATGTT TTATGTTATT 650
TACGACAAAT TATAATTGGA CTTTTTTAAT ACTCTTCACA ATCTTTTTTG 700
TGATTTTTAT TAAACATATT TCAAGAGTTT CTAACCCTTT TATTAATCCT 750
AAACTAGGGA AAAACATTCC GTTTATGCTT GGTTTGTTTT CTGGTGGGCT 800
AATATTTTCT ATAGTAGCTG GTTTTATATC AATGGTGCCT TATATGATGA 850
AAACTATTTA TCATGTAAAT GTAGCGACAA TAGGTAATAG TGTTATTTTT 900
CCTGGAACCA TGAGTGTTAT TGTTTTTGGT TATTTTGGTG GTTTTTTAGT 950
GGATAGAAAA GGATCATTAT TTGTTTTTAT TTTAGGATCA TTGTCTATCT 1000
CTATAAGTTT TTTAACTATT GCATTTTTTG TTGAGTTTAG TATGTGGTTG 1050
ACTACTTTTA TGTTTATATT TGTTATGGGC GGATTATCTT TTACTAAAAC 1100
AGTTATATCA AAAATAGTAT CAAGTAGTCT TTCTGAAGAA GAAGTTGCTT 1150
CTGGAATGAG TTTGCTAAAT TTCACAAGTT TTTTATCAGA GGGAACAGGT 1200
ATAGCAATTG TAGGAGGTTT ATTGTCACTA CAATTGATTA ATCGTAAACT 1250
AGTTCTGGAA TTTATAAATT ATTCTTCTGG AGTGTATAGT AATATTCTTG 1300
TAGCCATGGC TATCCTTATT ATTTTATGTT GTCTTTTGAC GATTATTGTA 1350
TTTAAACGTT CTGAAAAGCA GTTTGAATAG 1380

2) INFORMATION FOR SEQ ID NO: 229

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1365 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: HUC19
(C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

```
ATGAGAATAG TGAATGGACC AATAATAATG ACTAGAGAAG AAAGAATGAA        50
GATTGTTCAT GAAATTAAGG AACGAATATT GGATAAATAT GGGGATGATG       100
TTAAGGCTAT TGGTGTTTAT GGCTCTCTTG GTCGTCAGAC TGATGGGCCC       150
TATTCGGATA TTGAGATGAT GTGTGTCATG TCAACAGAAG AAGCAGAGTT       200
CAGCCATGAA TGGACAACCG GTGAGTGGAA GGTGGAAGTG AATTTTGATA       250
GCGAAGAGAT TCTACTAGAT TATGCATCTC AGGTGGAATC AGATTGGCCT       300
CTTACACATG GTCAATTTTT CTCTATTTTG CCGATTTATG ATTCAGGTGG       350
ATACTTAGAG AAAGTGTATC AAACTGCTAA ATCGGTAGAA GCCCAAACGT       400
TCCACGATGC GATTTGTGCC CTTATCGTAG AAGAGCTGTT TGAATATGCA       450
GGCAAATGGC GTAATATTCG TGTGCAAGGA CCGACAACAT TTCTACCATC       500
CTTGACTGTA CAGGTAGCAA TGGCAGGTGC CATGTTGATT GGTCTGCATC       550
ATCGCATCTG TTATACGACG AGCGCTTCGG TCTTAACTGA AGCAGTTAAG       600
CAATCAGATC TTCCTTCAGG TTATGACCAT CTGTGCCAGT TCGTAATGTC       650
TGGTCAACTT TCCGACTCTG AGAAACTTCT GGAATCGCTA GAGAATTTCT       700
GGAATGGGAT TCAGGAGTGG ACAGAACGAC ACGGATATAT AGTGGATGTG       750
TCAAAACGCA TACCATTTTG AACGATGACC TCTAATAATT GTTAATCATG       800
TTGGTTACGT ATTTATTAAC TTCTCCTAGT ATTAGTAATT ATCATGGCTG       850
TCATGGCGCA TTAACGGAAT AAAGGGTGTG CTTAAATCGG GCCATTTTGC       900
GTAATAAGAA AAAGGATTAA TTATGAGCGA ATTGAATTAA TAATAAGGTA       950
ATAGATTTAC ATTAGAAAAT GAAAGGGGAT TTTATGCGTG AGAATGTTAC      1000
AGTCTATCCC GGCATTGCCA GTCGGGGATA TTAAAAAGAG TATAGGTTTT      1050
TATTGCGATA AACTAGGTTT CACTTTGGTT CACCATGAAG ATGGATTCGC      1100
AGTTCTAATG TGTAATGAGG TTCGGATTCA TCTATGGGAG GCAAGTGATG      1150
AAGGCTGGCG CTCTCGTAGT AATGATTCAC CGGTTTGTAC AGGTGCGGAG      1200
TCGTTTATTG CTGGTACTGC TAGTTGCCGC ATTGAAGTAG AGGGAATTGA      1250
TGAATTATAT CAACATATTA AGCCTTTGGG CATTTTGCAC CCCAATACAT      1300
CATTAAAAGA TCAGTGGTGG GATGAACGAG ACTTTGCAGT AATTGATCCC      1350
GACAACAATT TGATT                                           1365
```

2) INFORMATION FOR SEQ ID NO: 230

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: HUC19
(C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

```
ATGGGGGTTT CTTTTAATAT TATGTGTCCT AATAGTAGCA TTTATTCAGA      50
TGAAAAATCA AGGGTTTTAG TGGACAAGAC AAAGAGTGGA AAAGTGAGAC     100
CATGGAGAGA AAAGAAAATC GCTAATGTTG ATTACTTTGA ACTTCTGCAT     150
ATTCTTGAAT TTAAAAAGGC TGAAAGAGTA AAAGATTGTG CTGAAATATT     200
AGAGTATAAA CAAAATCGTG AAACAGGCGA AAGAAAGTTG TATCGAGTGT     250
GGTTTTGTAA ATCCAGGCTT TGTCCAATGT GCAACTGGAG GAGAGCAATG     300
AAACATGGCA TTCAGTCACA AAAGGTTGTT GCTGAAGTTA TTAAACAAAA     350
GCCAACAGTT CGTTGGTTGT TTCTCACATT AACAGTTAAA AATGTTTATG     400
ATGGCGAAGA ATTAAATAAG AGTTTGTCAG ATATGGCTCA AGGATTTCGC     450
CGAATGACGC AATATAAAAA AATTAATAAA AATCTTGTTG GTTTTATGCG     500
TGCAACGGAA GTGACAATAA ATAATAAAGA TAATTCTTAT AATCAGCACA     550
TGCATGTATT GGTATGTGTG GAACCAACTT ATTTTAAGAA TACAGAAAAC     600
TACGTGAATC AAAAACAATG GATTCAATTT TGGAAAAAGG CAATGAAATT     650
AGACTATGAT CCAAATGTAA AAGTTCAAAT GATTCGACCG AAAAATAAAT     700
ATAAATCGGA TATACAATCG GCAATTGACG AAACTGCAAA ATATCCTGTA     750
AAGGATACGG ATTTTATGAC CGATGATGAA GAAAAGAATT TGTAACGTTT     800
GTCTGATTTG GAGGAAGGTT TACACCGTAA A                         831
```

2) INFORMATION FOR SEQ ID NO: 231

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4193 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: N315
(C) ACCESSION NUMBER: Extracted from AP003129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

```
ATGAGCCGCT TGATACGCAT GAGTGTATTA GCAAGTGGTA GTACAGGTAA      50
CGCCACTTTT GTAGAAAATG AAAAAGGTAG TCTATTAGTT GATGTTGGTT     100
TGACTGGCAA GAAAATGGAA GAATTGTTTA GTCAAATTGA CCGTAATATT     150
CAAGATTTAA ATGGTATTTT AGTAACCCAT GAACATATTG ATCATATTAA     200
AGGATTAGGT GTTTTGGCGC GTAAATATCA ATTGCCAATT TATGCGAATG     250
AAAAGACTTG GCAGGCAATT GAAAAGAAAG ATAGTCGCAT CCCTATGGAT     300
CAGAAATTCA TTTTTAATCC TTATGAAACA AAATCTATTG CAGGTTTCGA     350
TGTTGAATCG TTTAACGTGT CACATGATGC AATAGATCCG CAATTTTATA     400
TTTTCCATAA TAACTATAAG AAGTTTACGA TTTTAACGGA TACGGGTTAC     450
GTGTCTGATC GTATGAAAGG TATGATACGT GGCAGCGATG CGTTTATTTT     500
TGAGAGTAAT CATGACGTCG ATATGTTGAG AATGTGTCGT TATCCATGGA     550
AGACGAAACA ACGTATTTTA GGCGATATGG GTCATGTATC TAATGAGGAT     600
GCGGGTCATG CGATGACAGA TGTGATTACA GGTAACACGA AACGTATTTA     650
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CCTATCGCAT TTATCACAAG ACAATAACAT GAAAGATTTG GCGCGTATGA      700
GTGTTGGCCA AGTATTGAAC GAACACGATA TTGATACGGA AAAAGAAGTA      750
TTGCTATGTG ATACGGATAA AGCTATTCCA ACGCCAATAT ATACAATATA      800
AATGAGAGTC ACCCTATAAA GTTCGGCACT GCTGTGAGAC GACTTTATCG      850
GGTGCTTTTT TATGTTATTG GTGGGAAATG GCTGTTGTTG GAATTAAGGT      900
TCTATTTGAA ATGTAAAAAA TAATTCGATA TTAAATGTAA TTTATAAATA      950
ATTTACATAA AATCAATCAT TTTAATATAA GGATTATGAT AATATATTGG     1000
TGTATGACAG TTAATGGAGG GAACGAAATG AAAGCTTTAT TACTTAAAAC     1050
AAGTGTATGG CTCGTTTTGC TTTTTAGTGT GATGGGATTA TGGCAAGTCT     1100
CGAACGCGGC TGAGCAGTAT ACACCAATCA AAGCACATGT AGTAACAACG     1150
ATAGACAAAG CAACAACAGA TAAGCAACAA GTAACGCCAA CAAAGGAAGC     1200
GGCTCATCAA TTTGGTGAAG AAGCGGCAAC CAACGTATCA GCATCAGCAC     1250
AGGGAACAGC TGATGAAATA AACAATAAAG TAACATCCAA CGCATTTTCT     1300
AACAAACCAT CTACAGCAGT TTCAACAAAA GTAAACGAAA CGCACGATGT     1350
AGATACACAA CAAGCCTCAA CACAAAAACC AACTCAATCA GCAACATTCA     1400
CATTATCAAA TGCTAAAACA GCATCACTTT CACCACGAAT GTTTGCTGCC     1450
AATGTACCAC AAACAACAAC ACATAAAATA TTACATACAA ATGATATCCA     1500
TGGCCGACTA GCCGAAGAAA AAGGGCGTGT CATCGGTATG GCTAAATTAA     1550
AAACAATAAA AGAACAAGAA AAGCCTGATT TAATGTTAGA CGCAGGAGAC     1600
GCCTTCCAAG GTTTACCACT TTCAAACCAG TCTAAAGGTG AAGAAATGGC     1650
TAAAGCAATG AATGCAGTAG GTTATGATGC TATGGCAGTG GGTAACCATG     1700
AATTTGACTT TGGATACGAT CAGTTGAAAA AGTTAGAGGG TATGTTAGAC     1750
TTCCCGATGC TAAGTACTAA CGTTTACAAA GATGGGAAAC GCGCGTTTAA     1800
GCCTTCAACA ATTGTAACGA AAAATGGTAT TCGTTATGGA ATTATTGGCG     1850
TAACGACACC AGAAACAAAG ACGAAAACAA GACCTGAGGG CATTAAAGGT     1900
GTTGAATTTA GAGATCCATT ACAAAGTGTG ACAGCAGAAA TGATGCGTAT     1950
TTATAAAGAC GTAGATACAT TTGTTGTTAT ATCACATTTA GGGATTGATC     2000
CTTCAACACA AGAAACATGG CGTGGTGATT ACTTAGTGAA ACAATTAAGT     2050
CAAAATCCAC AATTGAAGAA ACGTATTACA GTCATTGATG GTCATTCACA     2100
TACCGTACTT CAAAATGGTC AAATTTATAA CAATGATGCA TTAGCACAAA     2150
CAGGTACAGC ACTTGCGAAT ATCGGTAAGG TTACATTTAA TTACCGCAAT     2200
GGAGAGGTAT CAAATATTAA ACCGTCATTG ATTAATGTTA AAGACGTTGA     2250
AAATGTAACA CCGAACAAAG CATTAGCTGA ACAAATTAAT CAAGCTGATC     2300
AAACATTTAG AGCACAAACA GCAGAGGTTA TTATTCCAAA TAATACCATT     2350
GATTTCAAAG GAGAAAGAGA TGACGTTAGA ACGCGTGAAA CAAATTTAGG     2400
AAACGCGATT GCAGATGCTA TGGAAGCGTA TGGCGTTAAG AATTTCTCTA     2450
AAAAGACTGA CTTTGCCGTG ACAAATGGTG GAGGTATTCG TGCCTCTATC     2500
GCAAAAGGTA AGGTGACACG CTATGATTTA ATCTCAGTAT TACCATTTGG     2550
AAATACGATT GCGCAAATTG ATGTAAAAGG TTCAGACGTC TGGACAGCTT     2600
TCGAACATAG TTTAGGTGCA CCAACAACAC AAAAAGACGG TAAGACAGTA     2650
TTAACAGCGA ATGGCGGTTT ACTACATATC TCTGATTCAA TTCGTGTTTA     2700
CTATGATATG AATAAACCGT CTGGCAAACG AATTAACGCT ATTCAAATTT     2750
TAAATAAAGA GACAGGTAAG TTTGAAAATA TTGATTTAAA ACGTGTATAT     2800
CATGTAACGA TGAATGACTT CACAGCATCA GGTGGCGACG GATATAGTAT     2850
GTTCGGTGGC CCTAGAGAAG AAGGTATTTC ATTAGATCAA GTACTAGCAA     2900
GTTATTTAAA AACAGCTAAC ATAGCTAAGT ATGATACGAC AGAACCACAA     2950
CGTATGTTAT TAGGTAAACC AGCAGTAAGT GAACAACCAG CTAAAGGACA     3000
ACAAGGTAGC AAAGGTAGTG AGTCTGGTAA AGATGTACAA CCAATTGGTG     3050
ACGACAAAGC GATGAATCCA GCGAAACAAC CAGCGACAGG TAAAGTTGTA     3100
TTGTTACCAA CGCATAGAGG AACTGTTAGT AGCGGTACAG AAGGTTCTGG     3150
TCGCACATTA GAAGGAGCTA CTGTATCAAG CAAGAGTGGG AACCAATTGG     3200
TTAGAATGTC AGTGCCTAAA GGTAGCGCGC ATGAGAAACA GTTACCAAAA     3250
ACTGGAACTA ATCAAAGCTC AAGCCCAGCA GCGATGTTTG TATTAGTAGC     3300
AGGTATAGGT TTAATCGCGA CTGTACGACG TAGAAAAGCT AGTTAAAATA     3350
TATTGAAAAC AATACTACTG TATTTCTTAA ATAAGAGGTA CGGTAGTGTT     3400
TTTTTATGGA AAAAAGCTAT AAACGTTGAT AAACATGGGA TATAAAAACG     3450
GGGATAAGTA ATAAGACATC AAGGTGTTTA TCCACAGAAA TGGGGATAGT     3500
TATCCAGAAT TGTGTACAAT TTAAAGAGAA ATACCCACAA TGCCCACAGA     3550
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GTTATCCACA AATACACAAG TTATACACTA AAAATTGGGC ATAAATGTCA      3600
GGAAAATATC AAAAACTGCA AAAAATATTG GTATAATAAG AGGGAACAGT      3650
GTGAACAAGT TAATAACTTG TGGATAACTG GAAAGTTGAT AACAATTTGG      3700
AGGACCAAAC GACATGAAAA TCACCATTTT AGCTGTAGGG AAACTAAAAG      3750
AGAAATATTG GAAGCAAGCC ATAGCAGAAT ATGAAAAACG TTTAGGCCCA      3800
TACACCAAGA TAGACATCAT AGAAGTTCCA GACGAAAAAG CACCAGAAAA      3850
TATGAGCGAC AAAGAAATTG AGCAAGTAAA AGAAAAAGAA GGCCAACGAA      3900
TACTAGCCAA AATTAAACCA CAATCCACAG TCATTACATT AGAAATACAA      3950
GGAAAGATGC TATCTTCCGA AGGATTGGCC CAAGAATTGA ACCAACGCAT      4000
GACCCAAGGG CAAAGCGACT TTGTATTCGT CATTGGCGGA TCAAACGGCC      4050
TGCACAAGGA CGTCTTACAA CGCAGTAACT ACGCACTATC ATTCAGCAAA      4100
ATGACATTCC CACATCAAAT GATGCGGGTT GTGTTAATTG AGCAAGTGTA      4150
TAGAGCATTT AAGATTATGC GTGGAGAAGC ATATCATAAA TGA             4193
```

2) INFORMATION FOR SEQ ID NO: 232

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2996 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

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ATGAAACGAG CCATTGGTTA TTTGCGCCAA AGTACAACGA AACAACAATC        50
ACTCCCAGCT CAAAAGCAAG CAATAGAATT ATTAGCTCCA AAGCACAATA       100
TTCAAAATAT CCAATACATT AGTGATAAGC AATCAGGCAG AACAGATAAT       150
CGAACAGGCT ATCAACAAGT CACCGAACGC ATCCAACAAA GACAATGTGA       200
CGTATTATGT TGTTATCGCT TGAATCGACT TCATCGCAAC TTGAAAAATG       250
CATTAAAACT CATGAAACTC TGTCAAAAAT ATCATGTTCA TATTCTAAGT       300
GTTCATGATG GCTATTTTGA TATGGATAAA GCGTTTGATC GCCTAAAACT       350
CAATATATTC ATGAGTCTGG CTGAACTTGA ATCCGATAAT ATTGGAGAAC       400
AAGTCAAAAA TGGACTTAGA GAAAAGGCAA AACAAGGTAA ACTCATAACG       450
ACCCATGCGC CTTTCGGTTA TCACTATCAA AATGGTACTT TCATCATTAA       500
TAATGATGAA TCACCTACCG TCAAAGCTGT ATTCAATTAT TATCTTCAAG       550
GATATGGCTA CAAGAAGATT GCACAATATT TAGAAGACGA TAATAAACTT       600
ATTACCCGCA AGCCTTATCA GGTACGAAAT ATAATTATGA ACCCAAATTA       650
TTGTGGTCGT GTCATCAATC AATATGGTCA ATATAACAAT ATGGTACCAC       700
CTATTGTTTC GGCAACGAAA TATGAACATG CTCAAGCAAT CCGTAATAAG       750
AAGCAACTTC ACTGTATACC TTCAGAGAAT CAGCTGAAAC AAAAGATCAA       800
ATGTCCTTGT TGTGACTCAA CACTGACAAA TATGACAATA AGAAAAAAAC       850
ATACATTGCG ATATTATATT TGTCCTAAAA ATATGAATGA ATCTCGCTTT       900
GTCTGTTCAT TCAAAGGAAT AAATGCACAA AAATTAGAAG TTCAAGTCTT       950
AGCTACATGT CAGAACTTCT TTCAAAACCA ACAGCTCTAT TCAAAAATTA      1000
ATAATGCAAT TCATCAACGC CTCAAAAAAC AAAGAGTGAT AGAAGCTAAA      1050
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AATTCGCATT ACAAAAAATA AAGCCCTTGT TGGGATCTAT TTCAAAAATG      1300
AACCATTGAA CATTGTGAAC CAAACCTCGC AATCATCGAT TGCTTAATCA      1350
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TATGTTCGTG TATCAACGGA AATCCAAAGT ACTGAAGGCT ATAGTATCGA      1450
TGGACAAATC AATCAAATTC GAGAATATTG TGATTTCAAT AACTTTGTTG      1500
TTGTAGATGT ATACGCGGAT AGAGGTATCT CTGGAAAATC TATGAACCGA      1550
CCAGAACTAC AACGTTTGTT AAAAGATGCG AACGAAGGTC AGATTGATTC      1600
TGTTATGGTC TACAAAACAA ACCGACTAGC ACGTAACACT TCTGACTTAC      1650
TCAAAATTGT TGAAGACCTT CATCGTCAAA ATGTCGAATT CTTCAGCTTA      1700
TCTGAGCGTA TGGAAGTCAA TACAAGCAGT GGTAAATTGA TGCTACAAAT      1750
TCTAGCGAGT TTTTCAGAAT TTGAAAGAAA TAATATTGTC GAAAATGTAT      1800
TCATGGGTCA AACCCGACGC GCTCAAGAAG GCTATTATCA AGGCAATTTG      1850
CCGCTGGGCT ATGACAAAAT ACCGGATAGC AAGCATGAAC TCATGATAAA      1900
CCAACATGAA GCGAATATTG TCAAATATAT ATTTGAGTCA TATGCTAAAG      1950
GCCACGGATA TCGTAAAATT GCGAATGCAC TCAATCACAA AGGATACGTG      2000
ACTAAAAAAG GAAAGCCTTT CAGTATTGGT TCAGTGACCT ATATCTTATC      2050
TAATCCATTC TATGTTGGTA AAATTCAATT CGCAAAGTAC AAAGATTGGA      2100
ATGAAAAGCG TCGTAAAGGG CTGAATGATA AACCAATAAT AGCTGAAGGT      2150
AAGCATTCCC CTATTATTAT TCAAGACTTA TGGGATAAAG TCCAATTACG      2200
TAAAAAACAA GTCAGTCAAA AACCTCAAGT CCACGGTAAA GGAACTAATC      2250
TATTAACAGG TATCGTTCAT TGTCCACAAT GTGGTGCACC AATGGCAGCT      2300
AGTAACACAA CGAACACATT GAAAGATGGT ACCAAGAAGC GAATACGTTA      2350
TTATTCTTGC AGTAACTTCC GAAACAAAGG CTCAAAAGTA TGTTCTGCGA      2400
ATAGCGTTAG AGCTGATGTG ATTGAGAAAT ACGTCATGGA TCAAATACTC      2450
GAAATTGTCA AAAGTGATAA AGTCATTAAC CAAGTCTTAG AACGTGTCAA      2500
TCAAGAAAAT AAAGTCGATA TTGGTGCATT GAACCACGAT ATCGCTTATA      2550
AACAACAACA ATACGATGAA GTCAGCGGGA AACTCCATAA TTTAGTTAAA      2600
ACCATTGAAG ATAATCCGGA CCTAACATCT GCATTGAAAG CAACTATTCA      2650
TCAATATGAA ACACAACTCA ATGACATTAC AAATCAAATG AATCAACTCA      2700
AACAGCAACA AAATCAAGAG AAACTATCTT ATGATACGAA ACAAATCGCT      2750
GCCCTATTAC AACGAATATT TCAAAATATA GAATCAATGG ATAAAGCACA      2800
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ACGGTAATCA TAAAAAACAG TTCTACGTTA CACTAAAACT CAATAATGAA      2900
ATTATTAAAC AACTTTTCAA TAATACCCCT CTCGACGAAG TGCTCCTCAG      2950
CACTTCGTCT TTATTTTTGC CTCAAACGCT CTTTCTTCAA ATCTAA          2996
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2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1410 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

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GCTGTAGGGA AACTAAAAGA GAAATATTGG AAGCAAGCCA TAGCAGAATA      50
TGAAAAACGT TTAGGCCCAT ACACCAAGAT AGACATCATA GAAGTTCCAG     100
ACGAAAAAGC ACCAGAAAAT ATGAGCGACA AAGAAATTGA GCAAGTAAAA     150
GAAAAAGAAG GCCAACGAAT ACTAGCCAAA ATTAAACCAC AATCCACAGT     200
CATTACATTA GAAATACAAG GAAAGATGCT ATCTTCCGAA GGATTGGCCC     250
AAGAATTGAA CCAACGCATG ACCCAAGGGC AAAGCGACTT TGTATTCGTC     300
ATTGGCGGAT CAAACGGCCT GCACAAGGAC GTCTTACAAC GCAGTAACTA     350
CGCACTATCA TTCAGCAAAA TGACATTCCC ACATCAAATG ATGCGGGTTG     400
TGTTAATTGA GCAAGTGTAT AGAGCATTTA AGATTATGCG TGGAGAAGCA     450
TATCATAAAT GATGCGGTTT TTTCAGCCGC TTCATAAAGG GATTTTGAAT     500
GTATCAGAAC ATATGAGGTT TATGTGAATT GCTGTTATGT TTTTAAGAAG     550
CATATCATAA GTGATGCGGT TTTTATTAAT TAGTTGCTAA AAAATGAAGT     600
ATGCAATATT AATTATTATT AAATTTTGAT ATATTTAAAG AAAGATTAAG     650
TTTAGGGTGA ATGAATGGCT TATCAAAGTG AATATGCATT AGAAAATGAA     700
GTACTTCAAC AACTTGAGGA ATTGAACTAT GAAAGAGTAA ATATACATAA     750
TATTAAATTA GAAATTAATG AATATCTCAA AGAACTAGGA GTGTTGAAAA     800
ATGAATAAGC AGACAAATAC TCCAGAACTA AGATTTCCAG AGTTTGATGA     850
GGAATGGAAA AAAAGGAAAT TAGGTGAAGT AGTAAATTAT AAAAATGGTG     900
GTTCATTTGA AAGTTTAGTG AAAAACCATG GTGTATATAA ACTCATAACT     950
CTTAAATCTG TTAATACAGA AGGAAAGTTG TGTAATTCTG GAAAATATAT    1000
CGATGATAAA TGTGTTGAAA CATTGTGTAA TGATACTTTA GTAATGATAC    1050
TGAGCGAGCA AGCACCAGGA CTAGTTGGAA TGACTGCAAT TATACCTAAT    1100
AATAATGAGT ATGTACTAAA TCAACGAGTA GCAGCACTAG TGCCTAAACA    1150
ATTTATAGAT AGTCAATTTC TATCTAAGTT AATTAATAGA AACCAGAAAT    1200
ATTTCAGTGT GAGATCTGCT GGAACAAAAG TGAAAAATAT TTCTAAAGGA    1250
CATGTAGAAA ACTTTAATTT TTTATCTCCT AATTACACTG AACAACAAAA    1300
AATAGGTAAT TTCTTCAGCA AACTCGACCG CCAGATTGAG TTAGAAGAAG    1350
AGAAACTTGA ACTCTTATAG CAACAAAAGC GTGGATATAT TTCAGAAGAT    1400
TTTTCTCAAG                                               1410
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/CA 02/00824

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, MEDLINE, EMBL, EMBASE, PAJ, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ITO T ET AL: "Structural comparison of three types of staphylococcal cassette chromosome mec integrated in the chromosome in methicillin-resistant Staphylococcus aureus." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES MAY 2001, 'Online! vol. 45, no. 5, May 2001 (2001-05), pages 1323-1336, XP002238384 ISSN: 0066-4804 cited in the application page 1334, left-hand column, paragraph 3 -right-hand column, paragraph 2; figures 1,2; tables 1,2 page 1335, left-hand column, paragraph 2 page 1335, right-hand column, paragraph 2	1-20
X	-& DATABASE EMBL 'Online! 14 May 2001 (2001-05-14) retrieved from EBI	14,17,18

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 April 2003	24.09.03
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Rutz, B

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	Database accession no. AB037671 XP002238391 abstract ---	
X	DATABASE EMBL 'Online! 7 January 2000 (2000-01-07) retrieved from EBI Database accession no. AB014433 XP002238392 abstract ---	14,17,18
Y	EP 0 887 424 A (KAINOS LAB INC) 30 December 1998 (1998-12-30) page 3, line 2 - line 10 page 4, line 28 - line 35 page 6, line 30 - line 34; figures 1-3,5,8 ---	1-20
A	HIRAMATSU K ET AL: "Genetic Basis fo Molecular Epidemiology of MRSA" J INFECT CHEMOTHER, vol. 2, 1996, pages 117-129, XP001122060 cited in the application page 120, left-hand column, paragraph 2 -right-hand column, paragraph 1; figures 2,4 page 122, left-hand column, paragraph 1 page 123, right-hand column, paragraph 1 -page 124, left-hand column, paragraph 1 ---	
A	OLIVEIRA D C ET AL: "Genetic organization of the downstream region of the mecA element in methicillin-resistant Staphylococcus aureus isolates carrying different polymorphisms of this region." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUL 2000, vol. 44, no. 7, July 2000 (2000-07), pages 1906-1910, XP002238385 ISSN: 0066-4804 page 1906, left-hand column, paragraphs 1,2; figures 1,2; tables 2,3 page 1908, right-hand column, paragraphs 1,2 page 1909, left-hand column, paragraph 3 -right-hand column, paragraph 3 ---	
A	ITO T ET AL: "Cloning and nucleotide sequence determination of the entire mec DNA of pre-methicillin-resistant Staphylococcus aureus N315." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUN 1999, vol. 43, no. 6, June 1999 (1999-06), pages 1449-1458, XP002238386 ISSN: 0066-4804 ---	

-/--

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	KATAYAMA Y ET AL: "A new class of genetic element, staphylococcus cassette chromosome mec, encodes methicillin resistance in Staphylococcus aureus." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUN 2000, vol. 44, no. 6, June 2000 (2000-06), pages 1549-1555, XP002238387 ISSN: 0066-4804 ---	
A	KURODA M ET AL: "Whole genome sequencing of meticillin-resistant Staphylococcus aureus" LANCET THE, LANCET LIMITED. LONDON, GB, vol. 357, no. 9264, 21 April 2001 (2001-04-21), pages 1225-1240, XP004246103 ISSN: 0140-6736 page 1234, right-hand column, paragraph 3 page 1238, left-hand column, paragraph 3; figure 1 ---	
P,X	MA XIAO XUE ET AL: "Novel type of staphylococcal cassette chromosome mec identified in community-acquired methicillin-resistant Staphylococcus aureus strains." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, vol. 46, no. 4, April 2002 (2002-04), pages 1147-1152, XP002238388 April, 2002 ISSN: 0066-4804 cited in the application figures 1,2 & DATABASE EMBL 'Online! 21 November 2001 (2001-11-21) retrieved from EBI Database accession no. AB063172 abstract & DATABASE EMBL 'Online! 21 November 2001 (2001-11-21) retrieved from EBI Database accession no. AB063173 abstract --- -/--	1-20

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	OLIVEIRA D C ET AL: "The evolution of pandemic clones of methicillin-resistant Staphylococcus aureus: identification of two ancestral genetic backgrounds and the associated mec elements." MICROBIAL DRUG RESISTANCE (LARCHMONT, N.Y.) UNITED STATES 2001 WINTER, vol. 7, no. 4, January 2001 (2001-01), pages 349-361, XP009004903 ISSN: 1076-6294 cited in the application page 352, left-hand column, paragraph 4 -right-hand column, paragraph 5; figure 1; tables 2,3 page 355, left-hand column, paragraph 6 -right-hand column, paragraph 4 & DATABASE EMBL 'Online! 8 March 2002 (2002-03-08) retrieved from EBI Database accession no. AF411934 abstract & DATABASE GENBANK 'Online! 5 March 2002 (2002-03-05) retrieved from NCBI Database accession no. AF411935 abstract & DATABASE GENBANK 'Online! 5 March 2002 (2002-03-05) retrieved from NCBI Database accession no. AF411936 abstract	1-20

P,X	BABA TADASHI ET AL: "Genome and virulence determinants of high virulence community-acquired MRSA." LANCET. ENGLAND 25 MAY 2002, vol. 359, no. 9320, 25 May 2002 (2002-05-25), pages 1819-1827, XP002238389 ISSN: 0140-6736 page 1823, left-hand column, paragraph 2 -right-hand column, paragraph 1; figures 2-4; tables 1,2 & DATABASE EMBL 'Online! 27 May 2002 (2002-05-27) retrieved from EBI Database accession no. AP004822 abstract	1-20

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
P,A	HIRAMATSU KEIICHI ET AL: "The emergence and evolution of methicillin-resistant Staphylococcus aureus." TRENDS IN MICROBIOLOGY, vol. 9, no. 10, October 2001 (2001-10), pages 486-493, XP002238390 page 492, right-hand column, paragraph 2; figures 1-5; table 1 -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA 02/00824

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (all partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type iv, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type iv, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type iv

Invention 2: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type v, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type v, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type v

Invention 3: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type vi, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type vi, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type vi

Invention 4: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type vii, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type vii, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type vii

Invention 5: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type viii, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type viii, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type viii

Invention 6: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type ix, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type ix, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type ix

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 7: claim 1 (partially)

method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type x

Invention 8: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type i

Invention 9: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type ii

Invention 10: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type iii

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/CA 02/00824

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 0887424 A	30-12-1998	JP 9224700 A	02-09-1997
		AU 696462 B2	10-09-1998
		AU 1810997 A	10-09-1997
		CA 2218476 A1	28-08-1997
		EP 0887424 A2	30-12-1998
		US 6156507 A	05-12-2000
		WO 9731125 A2	28-08-1997